

CCAAATCGCCCGGTGCGGTGGTGACAGGGTCTCGGGCTAGTCAATGGCGTCCCGGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTCACAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTAATGCAATGTTTCTGACTCTCGTTTTTTTGGTGAAGTGGTGCCTGCCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAGATCCAAAATACGTTGCAT
TGTTGTGGTGTACCGGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCAATGTATCTGTGGGCCTATTCCCTCT
CTACCTTTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAAGTC
ACAACCTACTTACTGATGACCAAAAAACCTACACAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGCTGCGAGTGGGCTGAT
TCAATCAAGATGTATGTTTGTATGTTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

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FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1' of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNENYFSLLEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLLVFLVELVAAIVGVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

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FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGTGTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGTTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
GTTCCCTCTTTCCGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAAGTCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAAATTC
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAAACAGATGACAGTGTGACACCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CAAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTCTTGTCTGTCATCTACTTTGCTCTGGAATGTCTAAATGTTTC
TGTAGCAGAAAACAGATAAGCTATGATCTTTATTAGAG

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FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVVRPPRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKQ

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTTCAGCCATTGCGC
CCGACGCCCTCTGTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCTAACGGA
CAAGATGGAGGAAGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

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FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTCATGAAGTACAGAGGACACCATCTT
CTTGATTATATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
GCTAGGCCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAG
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC
AGAAGTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAGTTGGGGAGAAAGGTCTCTGGGGT
CTGATCAATAATGCTGGTGTCCCGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA
ATCGTTGGAGGGGGCTATACTCCATCCAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
GACATCAAAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAAACTGAAAGGCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTTTCTGGATACCTCTG
TCTCATATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT
ATTTAGGCTTTGCTGCTTGGTGTGATGTAAGGGAATTGAAAGACTTGCCCATTCAAAATG
ATCTTACCGTGGCTGCCCCGCTTATGGTCCCCAGATTTACAGTAACTTGTGAATGTT
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FIGURE 8

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><MW: 35227, pI: 8.97, NX(S/T): 3
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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVS SVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVK VIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGKNSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFFLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 9

GCGGGCTGTTGACGGCGCTGCC**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGGACTTCTGAGCGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTGCGCCACCCT
 GTAGTCATGTATCCCAACGCCGCCGCCCTCATCGGAGCTTCATCTCGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTGCTGCTGGAGGAAATGGA
 AGCAACTGTCGAGATTGCAAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTTGAAAAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAATTGCTGGGTAAACCAGCAATCCACCCGCTCTTACCAG
 CTCTCTCAGAAGGCGGACACCGACCCCTGAGAAGCTTACCTGAGATTTCGTACAGAAGACACAA
 AGACACATCCAGCGGGGACCACTCACCTGCAGATTAGACCCCAAGCCAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCCTGTGGATCCCCGCCCGGAGGAG
 ATCCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCAGCCGAG
 CTCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
 CACACCACTGCATCTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGCTCCTTCAGT
 GAGTGGTTTGGCCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAATTTACACTTTGAAAAGGACG
 TGGACGTCAACCTGTTTGAGAGCACGATCCGATCCTGGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCTGGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGGCTAATGCCCTGC
 CTTCAGAACACCATCCAAGATTCCCTTACTCGGATGTGAACATCGGACTGTGAGTTGGCCACC
 CGCCACGGTGGCCCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG
 GAGCTCTCCGCTCTACAGGGGATAAGAAGTTTCAGGAGGCTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGTGGAGACATACGTGAGGA
 AGCCATCGAGGGTGTGAGAAGCAGCCTGCTGCGGCACTCCGAGCCAGTAGAGCTACCTTTTG
 TGGGGGAGCTTGCCACGGGCCCTTCAGTGCCAAGATGGACCACTGGTGTGCTTCTGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCAGGA
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACTTCAACCTTTACCCCGAGCCGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTCGGGCCAGAGACCGTGGAGAGCCTGTTTCTACCTGTACCGCGCTCAGAGGGGA
 CCGCAAAATACCAAGGACTGGGCCCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAAGCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCCAAACCTGCTCAGCCTGGACGCCATCTGTTCAACACCGAAGCCCACTCTGCTCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCCGGTGGGCAGAGGACCTTG
 CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCT
 CTGAACTGGCTCTGGGCTCTCTCTGCTCTGTTAATCAGGACACCGTGAGGACAGTGA
 GGCGCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCTCTGTTCTC
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGCCGACCA
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGCTGACCGAGTGGACAGCCAGGTTGCAGC
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 CTCAGAGGCTGAGGCTCCAGGCTGGCTCTGGTGTTCAGGACAGCTCAGGATCCTC
 CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCT
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FIGURE 10

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><subunit 1 of 1, 699 aa, 1 stop
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IAGLKPANPPVLPAPOKADTFPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLTLIDALDTMWILGLRKEFEFA
RKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSIFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPRWTSSTVAEVTISIQLEFRELSTGDKKFQEAWEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGELAHGRFSKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVGTGRKYQDWG
WEILQSFSTRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

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FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC
CGCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGCGGCCCTCCCTCGGAAGTGTTCCGCTTTCACCTGTTCTGTGGC
CTGCCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCATCTACGTGTCAACCAGGTGGACCACCTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCTGTGTCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
GCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCGCACCTGCATGACCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCTGTTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
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GGACCCCCCTGCCTTCTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
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FIGURE 12

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GQGQETSGPPRACFPPEPPPEHWEEDASWGPRLAVLVFPRERFEELLVFVPHMRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSQHYRLCNGMSNRFWGWGREDDFYYRRIKGAGLQLFRPSGI
TTGYKTRFRLHDPAWRRDQKRIAAQKQEQFKVDREGGLNTVKYKHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
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FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

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PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAGGCCCGCTCCTCCGCGCCGCCATAAGGCTCCGGTCGCCGCTGG
 GCCCGCGCGCGTCTCTGCCCGCCGGGCTCCGGGCGGCCGCTAGGCCAGTGCGCCGCCG
 CTCGCCCCGAGGCCCGGCCCGCAGC**ATGG**AGCCACCCGGACGCCGGCGGGCCGCCGCGCA
 GCCGCCGCTGTTGCTCGCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGCG
 GCGGCGCGCCGCGCGCTGCCCGCGCGCTGCAAGCACGATGGCGGCCCGCCGAGGGGCTGGC
 AGGGCGCGCGCGCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT
 GCCCCAGATACTCTGCCAACCCGACGGTCACCCTGATTCTGAGTAACAATAGATATCCG
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 GACAAACAATCGAATAGGATGCTGAATGCAGACATATTTCGAGGACTCACCACCTCTGGTTC
 GGCTAAACCTTTCGGGGAATTTGTTTTCTTATTATCTCAAGGAACCTTTTGATTATCTTGCG
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 CACTCGAGGCCCAACAGTACAGGCGTGAAGCAGGAGCTGTTGACATGCGAGCCCTCCGCTT
 GAATTGCGCTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTGGAAGACAGCCCT
 TCCTTTCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGAAAGAACATGATTCACAAC
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 TTGAAAAATTTGGAAGATTACCAAGGAGGAAAAATCAAAGAGCTAGGTGACGTGATGGTT
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
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 GAGCTCACGTTTTATTCAACATATTACCCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
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 ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATTGTACATTCTGCAATCATTT
 AAGACTATTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTCGCAAAAATAACCTTATTA
 AAAGATTTTTTTTTCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACFTA
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGGCCTTTGATTCCCTTT
 CTTACATAAAAAATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATGATACT
 ATTGTTACATGTGAAAAAATTTATTGACTTAAAGTTTATTATTGTTTTTTTGCTCCT
 GATTTTAAAGACAATAAGATTGTTTCATGGGCCCTAAAGATATCATGAGCCTTTGGCACTGC
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT
 ATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTAAAAAAAGTATTTC
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 GACTACACTGTATTGAAGCAAAATAGAGGAGGCAACAACCTCAGACCCCTAATGGAACCACTAG
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 TACTTTATTCTGTCTTGTGCCCTCAATAATATCACAAACAATATTCAGTCAATTTAATGGC
 TGCATAATACTGATCCACAGGTGTTAGGTGTTCTGGTTTGTGCTGTGAGCACTCAATAATA
 TTGAATGAATGACGAAAAAAGAAAAA

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FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPDPTLPNRTVTLILSNNKISELKNGSFSGLSLERLDLRNNLISSIDPGA
FWGLSSLLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSEFQT
EYLLCDCNILLWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT
SHRQVVFEQDGLPFQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTLAGITA
YLQCTRNTHSGSIIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

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FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGGAAAAAGAAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTGTACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTTGGAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 19

CTGTCGTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGACCACCATCACAACCACCACGACGTATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGGCCCTTCTTGCCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTCTGTCCCACGGCCGTTTCGGGGACACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCGGCCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCGCCGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGTACCCATCCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGTGTGTC
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCAAGAGGCTCC
 CGTCCCCTCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCCCTTCTCTGTTTTCTCTTCTCTCCCTCCCTCCACCTTTTTCTTTCTCTCC
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCCTTCCCTTCTCTTGCTGT
 TTCTTCTCTGTGTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTTCTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTGTGCGCCAGGCTGGAG
 TGCAGTGGTGCCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTGCGGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCTCCCA
 CCCACCTCCAAAGGTGTGAGCTCACATCCACACCCCTTGACGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCCCACCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGTGGGGGTGGGTAGCTGGGATTGGGCCCTCTTTCT
 CCCAGTGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG
 CCCCCTGCGACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC
 CCACTGCCTAGAGCCATCTTAAAGGAAGCAGGGGTGGATGCCTTTCATCCCACTATTCT
 CTGTGGTATGAAAAAG

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FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSSHVKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSDLGGLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQFLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

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FIGURE 23

GGTTCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCACCTAATTTGTTTCCCT
GGCACCTCTCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCTTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCTGATTGTAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGGCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
AAGCCTACAAATGTTGGCCTTAGCCAAAATTCTGTTGATTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGAAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TTAAACCAATGAAAAATAAACCTATTCTTTGGAAAGTGAAAGCAAACTTAAACTCAGATAAA
GAAATATAACCACTCAAATCTCAAGCGAGTCATTCCTCTCTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCCACATCTACCAATTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTAAAACTCCTGATA
ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAACAGTCAGTAGCTTCAGTGGGTTTACCCTTAA
TCAAGAAAAACAACCTACAGCCTACCTTAAATTCACCAATAATTCAAACCTCTTTCCAA
ATAGCTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAGAAAGAAAAAC
GGATTCATTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAAGTCTGCGATTAGACA
ATGACCCGGAACCTTATGATGTGAGTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
GATTGAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTATCTA
CATCCTAGCCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTAAGTGTACAGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTCTTACAAATTTTGGCCATCTGAGGCATTACTAAGTAGCCCTTAAT
TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
TCACCATTACAGCCCTGCCTCATACTAAATAATAAAAATTAATCCACCAAAAATTTCTAAA
ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAGATTGCAT
TTTTCTTAAATGAAAAATTGAAAGGGTGCTTTTAAAGAAAATTGACTTAAAGCTAAAAGAG
GACATAGCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTTC
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCAGGAAAGTAATAGCT
CTTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGCTCTTAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSEFVSKVPWNA
PIADEDLLPISAHFNATPALSSNFWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTNNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDSEFSHRRLYDDRNEPVLRLDNAPEPYDVSEFGNSSYYNPTLNSDA
MPSEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

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FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCGAAGATTCACT**ATGG**TGAAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
AGGCGCGGCAAGACGTGGAGGCCCTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCTTTCATTATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
TCATGCCCCAAGAGCACCATTACCCTGGAGAGATGTGCTTTTTTGATTCTGAGGATCTTGCA
AATTCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCCTGAG
CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTGCTGGGGAAGTGC
TATCTGATGCCCCCTCAATACTTCTATTGTATTGCTCCAAAAAATCTGGTAGAGCTCTTTGG
CAAACCTGGCGAGTGCCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
AAGTCCTTCCGCCCTTCGTGCGCAGAGACCTCTGTGCGGTTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
AAAAAAAGGAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT
TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCCTTAAGTAAGCTCTTATTCATCTTATG
GTGGAGCAATTTTAAATTTGAAATATTTTAAATGTTTTTGAACTTTTTGTGTAAATATA
TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTCATTTTGTACAACCTTCTTGAATTTAGA
AATTACATCTTTGCAGTCTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
AATGCACAAAATTTGTGTAGGTGCTGAATGCTGTAAGGAGTTTTAGGTTGTATGAATTCACAA
CCCTATAATAAATTTTACTCTATACAAAAA

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FIGURE 26

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCLMTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPKKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGFIFYQLCNNRKSFRLRRRDLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

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FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCCAGAGCAGCCCCGGGCACACGACGACTCTCT
CTTCCAGCCCAGGTGCCCCCCACTCTCGCTCCATTGCGCGGGAGCACCCAGTCTGTACGCC
AAGGAACTGGTCTCTGGGGGCACCATGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
TTGTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGTAGTGGGAGGCCGAGGGCTCGTCGGCTCCTCCCCGAGCCTCC
CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG
GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
GTGGACAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCCGCAGCTCCAGGCCGACATCTTGGCCG
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
GTGGAGGCGAGGGGCGCAGAGGAAGAGGAGAAGGCGAGCCAGGAGGGGACCAGGAAGTCCA
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
AGGGGGCTGTGGTGGCCGTTGAGGGCCAAGGGAGCTGGAAGGGTCTCTTGTGTAGCCAG
GAAGCCCAGGGACAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG
TGTCTAAACAGTCTCTCCGGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACCTCCCC
GTGTATGAAAGGCCTTCAGCCCTGACTGCTTCTTGACACTCCCTCCTTGGCCTCCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCGGA
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCTACAGC
ACAGTCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCAAACTACTTTTTAAACA
GCTACAGGGTAAATCCTGCAGCACCCACTGTGAAAATACTGCTCTTAATTTTCTGAAGG
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAATCCTC
TCAAGCGCTCTCCAAGCACCCCGCCTGGGGGTGAGTTTCTCATCCGCTACTGTGCTGG
GATCAGGTTGAATGAATGGAATCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTTGAGGGGACCTCCACCTTGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTGTCTACACATTGTCTGGCAGCCTG
TGTCACAATATTCTGTCAGTCTCTGACAGGGAGCCTGGGCTCGTCTGCTTTAGGGAGGCT
CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA
AAGA

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FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGFSPPTNFLDGI VDFRQYVMLIAVVGSLAFLLMFIVCAA VITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGFVGPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

GTGACTCTGAGAAGCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCTTGGTGGGAGGAAGACACTCTGAGAGAGAGGGGGCTGGGCAGAGATG
 AAGTTCCAGGGGCCCTGGCTGCCTCCTGCTGGCCCTCTGCTTGGGCAGTGGGAGGGCTGG
 CCCCCTGCAGAGCGGAGAGGAAGCACTGGGACAAATATTGGGGAGGGCCCTTGGACATGGCC
 TGGGAGACGCCCTTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAGAGAGCCGAGGGGCAGCT
 GGCTCTAAAGTCAGTGAAGGCCCTTGCCAAAGGCCACGAGAGAAGCAGTTGGCATGGAGTCAG
 CAGGTTCCAGGCTTTGGCGCAGCAGATTGGTGGCAACAGGTCGGGGAAGCAGCCATG
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGGAAGATGTATTCCACACCGGAGCA
 GATGCTGTCCGGGCTCCTGGCAGGGGTGCCTGGCCACAGTGGTGTCTGGGAAACTTCTGG
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
 GTCTGGGGACTCCGTGGGTCCACGGATACCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
 CCTCAGGGAGCTCCTTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC
 TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAAGTGAAGGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACATGGCAGCAGCAGTGG
 TGGCAGTCAGCAGTGGCAGTCAGTGGCAGCAGTGGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGTGGAGCGGCGAGTGAATCTCTCTCGGGGA
 TCCAGCACCGGCTCCTCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGACATAAACC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGGAGCGGGGAATCTGGGATTCAGGGCTTCA
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGGGA
 GGCTCTGGAGACATTATCGGGGGCAGGGTCGAGCTGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGAGTCAATACTGTAACTCTGAGACGTCTCTGGGATGTTTAACTTTGACACTTTCT
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAGGACCAGAGA
 AGCTCTCCGATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT
 CCTCTCTTAAACACACCCTCTCATCTACTACTCAGCCCTTGCCCTTGAAATAAACCTTA
 GCTGCCCAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCCGCGGGCGGTGCTCACC
 TGCCTTGGCTGGTGGAGTTTCTCTCTCTTGTGACCATGTTGTTCCCTTGTGGAATATTACCGGGACATCTTCA
 CTCTCTCTGCTCGCCTGCACCGGAGCTTGGTGTGTGCGAGGAGTGAAGGGAAGATGTTGTTTCTGAAACAAGC
 TGTGCTACTTGTCTGCTCGGGTGGCTTTTCCAGATTCCCACAGTCCCTGAGGACTTGTCTTCTTGTGAAGAGG
 GTCCCTCATATGCCCTTGAAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGACCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACATGCTCGCTTCGTGGGTGTACGGCAGTAGTG
 GACGGAGTGGGGCTTATGAGGAAATCACCCCCACCACTACCAAGCTGGGAGGCCAGCTTCCCAGAGACA
 GCCAGGGGTGCAGGCACAGCTCGCCAGGCCCTTTTCCACAACAGCCGCCCTCTTGCGCCGAGCCGTAGAGT
 TCGTGGCAGAAAGATTTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCGAGATCTGGTGCCGACG
 CAGAGTCACTTCTCAAAGACAGCTGGTGACACAGGAGAGGAAGGGGGAGCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAGACAGCAG
 TGAGTCGCACACTTCAGGCCAGGGTCTTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAC
 GTGCTCTCTTGGCCGTGGGGCCACGGACCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTTAGCC
 CAGCTGGGGCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTCTCTGTG
 GAGTTAGCTTCCCTCTCGTTGCAGATCAAATTCCTATCTTAGGGCCCCGGACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGCTGTTTCTTGTGAAGGAAGACTTTCAGGGGGCGGTCCGCTGCAGTCT
 CTGCTGAGCCCAAGAAATGTGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGTGCTATTCTTGTCTA
 CGGGAGCTGGTGGAGAAGGCTGTGATGGGACGGATGGAGATAGAGGCTGCTTGGGACCCCTCCACACGGCCGAG
 TGGCCAGGGGACTTGTCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGCCCCACTCGGACCAACCC
 CAGCTAAGAGCCTGTGAGTTGTGTGAGCACAACCCGGGCACTGTGCTGGCCAGAGCTTAGGGCTGAGAATCTGCC
 CTGCTTGTGGCATTTGACCAAGAACCTGGACCCCGCCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCTCAC
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTACTGCTGGCATCCCACACGCCGA
 ATCTCAGGAAGAGAGAGTTGGCGCTTGTGGATTATGGCAGAAAGTCCAGAGATGCCAGCTCTGGATGAGAA
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAATGAGGTGTGTGGCTTGTCAACACAGAAATCTCAGCCT
 CATTTGCTATCCCAGCATCTCTTAAAGACTTTGTAGTCTTGAATTCATGACAGCAAAATGACTCTGCTTAAC
 TTTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTATACACAGGAGCTTAGAGCTGCCATCTCTT
 ATAAATGCTTAACACAGCCGGGTGTGGTGGCTATGCTGCTTAATCCCAGCATCTGAGAGGCTCAGGTCGCGG
 GACTGCTGAGGTGAGGAATTCAAGACACGCTGGCCACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTTATTAGCTGGGCATGGTGGTGTGTGCTCTGAATCCCAGCTACTCAGGAGGATGAGCGAGAGACTGCTTGAAC
 CTGGAGGTGGAGGTTGAGTGAGCCGAGGTGCACCACTGCACCTCAGTCTGGGTAAACAGAGAGACTTTCTAG
 AAAAGCCTTAACAAACAGATAAGGTAGGACTCAACCAACTGAACCTGACTTTTCCCCCTGTACCTTCAGCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGACCAAGCAAGGCACTTAGAGCTTTTAGAATAAA
 CTGGTTTCTTTTAAAAAAGGGGCTTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 TTTTCTTTTCTTTTAAAAAGGGCTTTTATTTAAATTTCTCCCAACAGATGGCTCTGCAATCTGCCACAGCTG
 TGGGCGGTGCTCTGAGGGAAGGCCCTGTTTCCCTGAGGCGGGCTGGGCTGTGCATGGGTCCCGGAGCTG
 CGCGTGTGTGGCGCCTGTGCGTGGTGTAGCTGCTTCTTGGCGGACAGAGCTGCGGGCTGTGGGGACACCGG
 AGCTAAGAGCAGGCTGTGTGTCAGGGGTGGAGGCTGTCTCTTAACCGACACCTGAGCTGCTCTGAGTGTGCTG
 GGTCCACCTCGAGTGGCAGCGGGAGCAGCTGTGGCCGCTGCTCTCTYTAGGCAGCTCTGGGGAACATAAGCTG
 GGGCCCTCTTTTGAAGACCCAGGATGGGTGGGTGGGGACTCAGGGGAATGGCTGAGGAGCTAGCGTGT
 GAAGAGGGCGCGGCTTTGTGGCTGCAGCGGCTGGAGCGCTCTCTCTGAGCCCTCACTTCTTCCCTTCGCTCTA
 ATGAAGAACATGCGCTCTGGTGTCTCAGGGCTCTAGAGACTTGCCTCAGGAAGTGGCTTGGACGCGGTCTCAT
 GTTATTCTTCCAACTGTCTGCGACGTTGGCCTGGGACGTCATGGAATGGCCATGGCCCTGCTGCTGCGTGTGCT
 GTGCGGCTGGAGAGTGGCAGGACAGGCGGGGCGCAGAGCTGGCGCTGAGGGAGGTGGCGGAGCGCCGGAAGG
 CCTCACAGGAAGTTGGGCTCCCGCACACAGCAGGCGGGCTCCCGCGGCGCGCGCCACCTGCTGCTGAGC
 GCGCGGTAGCAAAAGTGAAGTTCGCGCTTGGGCTGCTGCGCAGAGCTGAGCCCTTGATGTCAGTGGCGAGCGCG
 TCGTCCGCGAGCTGGAAGCAGCGCCGCTCCACAGCAGCAAGCAGCGGTGCGCCT

FIGURE 32

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPHEGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

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FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
AAGACTCTCTGCTTTTGGCCACAGCAGTTCCCTGCAGCTTCCCTTGAGGTGTGAACCCACATCCCC
TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
AGTAGCAACAAGAGCAGCGGTTCAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
CATCCTCTACAGCTCCAACAGTGCCAAATGAGGTCTTCCATTACGGCTCCTCGGGGGCCGTA
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCATTTCTCGGC
AACAGACACTGCCTCTCGGTGCCACCAAGTGTGTGATTGTACGACAGTCCAGCCACCTGCT
GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAAATCCGCATGAATGATGCAC
CCACCCTGGCTACTCAGCTGATGTGGGCAACAAGACCACTACCGCGCTGTGGCCCATCCT
AGTGTGTTCCGCGTGTCTGAGGAGGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
CATCTTCTGGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCTGTGATCC
AGCGAGCGGGCTGGTGTTCCTCCCAACATGGAAGCATATGCCGTCTCTCCGGCCCGCATGCGG
CAATTTGACGACCTCTTCCGGGGTGGAGCGGGCAGGACAGGGAGAACTCTCATTCGTGGTT
GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTACACAGTGCATGTCTATG
GCATGGTCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
TACGAGCCCCAAGGGGCCGACGAATGTGTACCTTACATCCGAATGAGCACAGTCCGAAGGG
CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
TCACCTTCTCCACCCCTCTCGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
AGGAGAAGCAGCCTCCGCCAGCGCGTAGGCCAGGGACCATCTTCTGGCCCAATCAAGGCTTG
CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
TGGGGAATCTGTTGGCAATCAGGGATTGGGAGTCTATGTGGTTAAATCAGGGGTGTCTTTCT
TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGAGTCAATCTG
AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAAGGCCCCAGGAATGAGACCCCCCA
ATCACTCCCCACTCTGCTGGGATAATGGGGTCCGTGCCAAGGAGCTGGGAACCTGGTGTG
CCCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
GGCCAGAGAATTTGTGGGGTGTGGAGGTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA
GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGACAAACCCCTCCCCCTCTCTGGG
CACCTTCTGCCACACCAAGTTTCCAGTGGGAGTCTGAGACCCCTTTCCACCTCCCCACAA
GTGCCCTCGGGTCTGTCTCCCGTCTGGACCTCCAGCCACTATCCCTTGTCTGGAAGGCT
CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCTCGGAAACCTTTAGGGTATTTTTCG
GCAAACCTCTCAGGGTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
TAGCCCCCTCAGCAGCTGCCATTAGCTTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT
CTAGCAGGGAGGTTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
CTGGGGGCTTCGAGGGTCTCCTCGACCTCTGTCTCTGGGATGGCTGTCTGGAGCTGT
ATCACCTGGGTCTGTGCCCTGGCTCTGTATCAGGCACCTTTATTAAGCTGGGCCCTCAGTGG
GGTGTGTTTGTCTCTGTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
GGCTGGAGGGAGAGATGGAGGAGGCCAGCAGCTAGCCATTGCACTGGGGTGTGGGTGG
GGCGGCTGACTGCCCCAGACTTGGTTTTGTAATGATTGTACAGGAATAACACACCTACGC
TCCGGAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 34

MSSNKEQRSADFVILFALITILILYSSNSANEVFHYGSLRGRSRFPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRFPQEFVNRTPETVFIFWGPPSKMQKPQGS�RVVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRRLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

TTCTTCTCATATCTGGCGTCTCTCTAAGGAAAAACACTAAATAGGAACATCAGCGGACGGGGGCGGACGACGCTTG
GAGGGAAGCATCTGACTGCTTGTGGCGACGAGGGCGAGGCTGAGCGCAGTGCGGCCGAGGTGTCTTGAGGGGCTGG
GGCAAAAGTGAAGAAAGTTTTCAGAACAGACTTCTGGAACCAAGTACGCCATGAAGTCTTGTGCATATTTATAACGT
CTGAGGTTAGACACTCGAAACTAGAGAAATGGAGTGTGCCAGGAGCGGACGATCTCTTTTGTGTGACCTGGC
GGCCTATGGGACCTTGGCTTCAGACCTTTGTGTATACACATCTCGTGGTGAGCATGACGGCTGGAGAGGAAATG
AGGCTCTGAGGTACACTTGGCTTGGCTCTCTAGCCACAGCGGCTGTTTGTGACTTGAACGAGTCTCCCTCAG
TGACCGCTCCAGCTTGGCTTCCACCTGCGGAAGCGCGGAGGACCTTGATCTTGGGCTGTGCTGTTGGAACCTCCA
AGATGAATGTACCTTGGCGCTGAATGGAAGAGGACTATAGTGCCTGCGATGATGCTTGGGTGTCTCTCTATCAC
GGGGTGTGGCGGCTGTGAGCGCTTTACACATCACCTTGTGGGACGAGCTGTGTGGCGCGGATGCTGGCTGG
TTAAGAATGGATGAGGAAACACAGCACTTATGCTGCCACTGCTGACAGCTGCTGCTCAAAACCGAGGTGCTG
TCAGCGCTCAAAACAGAGTGGCTGGAGGCGCTCAGAGTAACTACTCTGATACCTGCCCTCAGGGAACCTCAGATT
TGAATGGCCGACGAGGAGGACGAGGCAATGTACAGTGTGAGCCTGTAAACCAAGTACGCCAGGAGTGAACAA
CCCGCTCCAGGACAGGCTACGTTGGCGCGCTCCACCGTCTGAGGCTGCCGCAATCATCTACCTCCCCAGGAGCC
CAAAACATCATGTCACAAAGGCGCAGAGTCTATTCTGGAATGTGTGGCAGTGAATCCACCCCAACGGGTG
ACCTGGGCAAGGATGGGTCAAGTGCACCGCTCAACAAAGACGGCTTCTCTGTGAGCAACCTCTCTATGAGC
ACCAACGCGGAGGAGGACTAGGCACTACCGTGCATGGCAGCAATGGGTTGGGCAACCGGGGACGGCTG
ATCTCTACAATGTCAAGTGTGTTGACCCCTGAGGTACCCATGAGCTATCCAGCTGTGCTCTCTCTGGGG
CAGAGTGGCGAGCTTCTGTGAGGTGGTGGGAACCGCCGCTCGTGCTGTGGGTGAGGAATGCTGTGGCC
TGCTACAGTGCATGGCCAGTGGAGGTGTGGCGAGGCTCGCGCTCAGCATGGGGCTGAGGACAGAGGCT
ATAACCCCAAGGCTGTGGCAGATGTGACTGCTGCTGCGACACTCTGTATACCTCTCCAACTGCGCAAC
CCTGACGAGTCTGTGAGGGGCAACCGGCTCCCGAACCCCAACCTGACGTGGGGCTCTCTCCCGAATGTG
TCAGGAGAGAGGGGCAAGGGGCTCCCGCGAGGCTCCCATCATCTTCAAGTGCGCCCGCACTTCCAAGACAG
TCATATGAAGTGTGTGGCGGCTCGCATGAGGCGAGTGGCGGGCGCAATCTCTACTATGTGTGAACAC
CCCAATGAGCTCAAAATTTCTCTGACATGTGACCACTCTGCGATCTAGCCAAACGACCGGCTGACCTC
ACGACATGTGACCCGGGAGTGTATGGAAGTGGAGTGGCACTTACAATGTGCGGGAGAGGGGCAAGACGCC
ATGTTCACTTTCGCAATGGACGGCGGCAACCCAGATCTAGCGCAACAGAGACGAGATCAGAGAGAG
ACCTCTGAGCCGAGTCCGAGAGCAGGACAGCCAGCAACCGCGGCTCTCCCCCCAGAGATCCCGGACAGG
ACCACTCTCCAGGCTCTCGAGACTCATGTGTGATGACCTGGAATCCCGTGAGGATGTGGGTTCCCAATC
TGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
CTGGGGTGTCCGTGAGCATCAGCGGCTTAGAGAAAGCACTCTGAAGTTTGTGAGGCTGAGGCTGAGGCT
TGCGGGGAGGCGAGGCTAGCGCTCCCTCTCGGCTACTGTGTGTGCGGCTGAGGCTGCGCTGTACGAGAG
CCGCTGGCAGGTCTCTTATACACTTCAGGATCGGCTTAATGAGACCAACATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAAACACACACCCCAATCATGCTTTTATCTATCTACGCCACAGACAGTGAATGATGATG
GACTACAGAAAGATATGTTGGAAGGGGCAAGTACTGGCACTCATAGCCACTCGAGGACAGAGCTCTCTAC
GACATTAAGATGTCAAGTGTGATGAAGGAGGGAGGAGAGGTTGACAGACGTGATGATCTGTGAGACAAAGCT
CGGAAGTCTCTTGCGCAGCTGTGTCGACTGCGACCCCAACCTTGCCGCCACAGGCGGCCCTCTCTGAAAC
ATAGAGCGGCGCTGGGCACTGGGGCACTGTGGTGTGCTGCCAGGACAGCTGCCCTATCTGATTTGTGGGGTGTG
AGGAGTATCTGCTTCTCATCTGCACTCATCTCCCTCTCTGCTGTGTGAGGCGTGTGCTTAGCAAAAACAT
CCAGGCTAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
CATAGGGGCTGCCCTTCCGCTCTGCTGGCTGAGCTGAGCCGACATGGAACCCCAACAGCACTGCCAGCGAGCTTCAG
CAGAGAGTGACACACGACGCTGCTGAGGACAGCCATTTGGAATGGATAGACCCCAAAGTACAGAGAT
ACGAGGGGTTCCCAAGTCTAGCCCGCAGGAGGCTCTTTCTATACACTGCGCCGACAGCTCCACTACAGAGCT
CTGAGGCCCATCAGCACTGTGCCAACCCAGGAGAGGCTGTGCTGTGGGCACTCAGGGGTGAGGAGAGCC
CCGACAGTCTCTGTCTGGAAGCAAGTGTGGGACCTTCATTCTCATAGGCGGCCCATGCTGCTTGGGCTGTG
CCAGTTGAAGAGGTGAGCACTGCTGACTCTGCCAAGTGAATGGAGAGACTGGTGTCCCCAGAACCCGTAGGG
GCTCATGTAGGACAGGAACCTGGAATGACGCTTCCCCGGGCCACTGGTGCGTGTGCTCTTTGAACACCACT
TCAACAATTTAGGCAAGAGTGTATATGCAAGAGACTGATATATGTTTTTTTTAAAAAAAGAAAGAAAGAA
AGAGACAGAGAAATTTGGTATTTATTTCTATTAGCATATTTATATATTTATGACATCTGTAAGAAATGTA
GAGGAG
CTATACAGAGCTCACCGGCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
GAGGCGAGGCTCGAGGAGGCCACAGATAGCTGGCGAAGGAGAGGATCGCCAGCACTGTGATACGAGCTG
TAGGGAACACGACAGGGGACGGTATACAGCTGGAGACACCCACAGATGGCTGAGTCCGCTGTCCGGAA
ACATTTTCTTAGAGTCCGCTAGGAAACAGACCAAGATGTGACAGCACTATGACATATAAAAACCTTCCAGAT
CAATAACTCTGGACATATCTCTGTAAAAAAACCACTGTAACTTTAATAATGTTAGTCTTCCCTGTAAAA

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FIGURE 36

MLRGTMTAWRGMREVTILACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP
 RMNVWTRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSSGNLQ
 IVNASQDEDEGMKYCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFPEPVTMELSQLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTS SVGPASPKCPGKQGAPAEAPI ILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFTTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWHSHLQPETSYDIKMQCFNEGGESEFSNMV
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFLWRWSKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCQQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCGLGLVPVEEVDSPDSCQVSGGDWCPQHVPV GAYVGQEPGMQLSPGPLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCTGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTTCCCGCGC
GCTCAGCCGGCGGTATCTGCGCGCTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
CCGTAACCCGCGCGGAGACCACGCCGGGCCCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC
AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTACTACCCAGGCCTCCTACGCCAGG
CACCCCAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAGAATGTGCTTCAGGAT
GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC
TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAAGTTCGAGCTT
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTTCAGACAC
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAAGTAGTAGAGGAGTTGAA
CCGCTGGGCATGATGATAGATTTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCCCTGG
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAAATTTG
TTGAATGTTCGGATGATATCCTGCAGCTTCTGAAGAAGGTTGGCATCGTGATGGTGACACT
GTCCATGGGGGTGCTGCAGTGAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
ACCACATCAGGGCAGTCATTGGATCTGAGTTTCATCGGGATTGGTGGAATTTATGACGGGACT
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTTCGTGGAACCTGCTGCGGGTCT
TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCGTGGAGGCTGAGTTT
CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCCTCAGAATGGACACCAAGC
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCTCAATGCTC
CCCCATACCTTGTTCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCAACCAAGTGGCTC
TG**CTGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNLDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTTQWLK
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCACAGCCTGATAAGC**ATG**
AAGCTCTTATCTTTGGTGGCTGTGGTTCGGGTGTTGCTGGTGCCCCAGCTGAAGCCAACAA
GAGTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCT**TAGAT**GGGCTGG
TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCCTGTGGCATTCTTCCCTCCTT
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTCGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCCTTCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTCTTCA
GGAACTCAGTGTCTGGGAGGAAAGCATGGCCCGAGATTACGATGTGTTCCTTTCTGCAGTG
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCCTGGA
AGCTGGTGTTCGCTGTCCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGGTCCCCCTACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG
CACAGTCACTGAGCCGACGGTCGGTTGGAACATGAGACTCGAGCTGAGCGTGGATCTGAA
CACCACAGCCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACCTCGTTGTACCAAGTGCATGGA
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG
TTTTATTCTCTCA

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FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSKDCNCLHVVEPM
PVPGH DVEAYCLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGGTTGGGTTCCGCTAATTTCTGCTCTGAGCGGTGAGACTGAGTTCATAGGGTCTGGGTCGCCGA
 ACCAGGAAGGGTTGAGGGAACAACTTCGCAAGCCCCCGACCCCAAGTGAGGGGGCCCGGTGTGGGGTCTCTCCC
 TCCCTTTGCAATTCGCCCCCTCCGGGCTTTCGCTCTTCTGGGACCCCTCGCCGGGAGATGGCCCGGTTGATG
 CGGAGCAAGGATTCGTCTCTGCTGCTGCTCTACTTGGCCGGGGTCTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAAACTCAACTCCATCAAGTCTCTCTGGCGGGGAGACGCCTGGTCAGGCCGCAATCGATCTCGG
 GGCATTGACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGGCAAAACCTGGGCGAGGCTACCTCTGTAGACAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCAACCAAGGATCATCGGCTGCATGGTGTGTCGGAGA
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCACAGTACCCGCTGCAATAATGGCATCTGTATCCAGGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAACCGTCATTAC
 TCAACCATGACTTTGGGATGGCAGAACTAGGAAGACCACACACTAAGATGTACATATAAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTGCTATTCTGGACCAAAATCTGCAAA
 CCAGTGCTCCATCAGGGGGGAAGTCTGTACCAAAACACGCAAGAAGGGTCTCATGGGCTGGAATTTTCCAGGGT
 TGCAGCTGTGCGAAGGGCTGTCTTGCAAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGATTATTAATGCATTATAG
 CATGGTGGAAAAATAAGGTTAGATGCAGAAGAATGGCTAAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAGGGAGAAAGAAACATGAATGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATATG
 CAACTTGTCTATGTAAATATGTACACATTTGTGGAAAAATGCTATTATTAAGAGAACAGCACACAGTGGAAAT
 ACTGATGAGTAGCATGTGACTTCCAAGAGTTTAGGTGTGCTGGAGGAGAGGTTCCCTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAATACTCCTAGATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATGCTAAACAAGAAATGAAACATGGAGCATTTGTTAATTTACACAGAAAAAT
 TACCTTTTTGATTGTAACACTCTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAATCAGTCAAAAT
 TTCCAAATAAATGCAAAATAATGGCCAGTGTGTTAGGAAGGCCCTTTAGGAAGACAAATAAATAACAAACACAG
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTAACTGTAATTAATAAGAACTGATACAGACAAAAACAGTCTCC
 TTCAGATTCTCAGGAATGACAGTATATCTCTTTTATCTCTATGTGATTCTGCTGATGCATTATATATTTTCAA
 AACTATACCCATAAATTTGACTAGTATAAAATACTTACACAGAGCAGAAATTTCCACAGTGGCAAAAAATTTTCA
 GATGTCCAATATATGTGGGAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATTAACCTATATTTT
 GATAGAATTAGATTGGTAATACATGTATTCATACATCTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAAATGGGAAAACTTTTTCGTTTGTCTAGGTTTGGCAACACATAGATCATATGCTG
 AGGCACAAGTTGGCTGTTCATCTTTGAAACCAAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATATATTTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCCGTACTATCCTCAAAATATTTTATTTATAG
 TGCTGAGATCCTCAATAATCTCAATTTCAAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTTCTATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCAAACCTCTGCAGCATCTG
 TTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATAAAGTAGGATAACTTGTAA
 ACCTCGATATTGCTAATCTATAGACACCACAGTTCTCAAAATCTTTGAAACCACTTTTACTACTTTTTTTAAACTT
 AACTCAGTTCTAAATACTTTGCTGGAGCACAAAACATAAAAGGTTATCTTATAGTCTGACTTTTTAAACTTTTG
 TAGACCACAAATTCACCTTTTAGTTTTCTTTTACTTAAATCCCACTCTGCAGTCTCAAAATTTAAGTTCTCCGAGT
 AGATTGAGTTTGGAGCTGTATATCTATTAAAAATTTCAACTTCCCACATATTTTAACTAAGATGATTAAAGACTTA
 CATTTTCTGCACAGGTCGCAAAAAACAAAAATATAAACTAGTCCATCCAAAGAACCAAGTTTGTATAAACAGGT
 TGCTATAAGCTTGTGAAATGAAATGGAAACATTTCATCAACCAATTCCTATATAACAAATATTATATTATTTACAAT
 TTTGGTTCTGCAATATTTTCTTATGTCCACCCTTTTTAAAAATATTATTTGAAGTAATTTATTACAGGAATG
 TTAATTGAGATGATTTTCTTATAGATATTTCTTACAGAAAGCTTTGAGCAGAAATATTTCGACGATATTGAC
 TTTGTAATTTAGGAAAAATGTATAATAGATAAACTATTAAATTTTTCTCTCTTAAAACTGAAAAAATAA
 AAAAAAAAAAAAAAAAAA

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FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
 FGGSKKGKNLQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN
 GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLR
 SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
 SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTTGGCCTCCCAAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGA
 TAGTGCATTATTATTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGACACCACAAAAATGGCAACA
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCACTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCTCT
 CCTGGTTTGGAGTCTTTCTTCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCAGCAGCAGCAATTGAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAACACATCAAACCTGCTAAGCGGGCGGATACCCCCAGCTTCTAAG
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCACTGCAGTACAGAACTCCACATATACAACCTCCGTCAATACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCCTGTGCATAACAGGATCCCATAACCAAGCCCTGTGAGTTCATCAGAGTCAGTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCTGGCTGGTGCCAACCAACAGAGGAAGGATAGCTCAGGTGA
 TGTGGAACCAACAGTTGGTCAATGGCTCATTCGTTAAAAAGCAGCCCTTTTGCTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAAGCACCCCTGGGCAACATGGTGAACTC
 TGCTCTACTAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAA

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FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
 PSTQQNSTSHPTTTTSDWLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP
 PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIIKLAKRRIPPASK
 IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPIISLYSKSLSEPLNT
 SLSMTSAVQNSTYTTT SVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
 GTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACCTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACCTGGGACCGGCAGCCGCCGGG
 GTCCCGCAGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA
 CGGGCCCTTTTTCTGCGGACCGCGTGGCTGTGGGCGGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTGCGCCGAACCCACGC
 GGAGCGCCCCCCCCGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCGTCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGTGGGCTACGTGCTGGCCACGCTGCTGCTTTCATCTGCTACTGTGTAC
 TGTCTCCTGGCGCCCGCAGGCGCCGCGGAGGCTACGAATACTCGGACCGAAGTCGGGAA
 AGTCAAAGGGAAAGGATGTTAACTTGGCGGAGTTCGCTGTGGTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAA**ATAG**GAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCGCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAACC
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGGTCAGCCTCA
 GGGCAGGAGTCCCATCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTTGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTGGGGTGGCCTGTGTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

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FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
 PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRVVEEAQQVVHWDRQPPGVPHDRADRLDL
 YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
 HLTVAEPHAEPPPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
 LLFILLLVTVLLAARRRRGGYEYSQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
 NILKERAELAHSPLPAKYIDLKGFRENCK

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCAC**ATG**GCCGTGTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCCTTCT
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT
ATCACTGCCAAGGAGTACTGGATGTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCAGGGGA
GGACCCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGGCCGTTCCTCCACCG
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC
CGTGCTCTGGCCTCACTGACGGTCACTCCTGGCCATCTTCATGGTGATAACTGCAGTGGTGAA
GGTGGACACTTCTCCTGGACCCGCTGGTTTTTTTGGCGTCACCATGGTCTGCATGGTGATCC
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATACCGGCTCCTTTCTCTATG
AGGAACTCCCAAGCACTGATATCAGGAGGACCATGGGCGGACGGTCAAGCCGCTGGCCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCTGTTCTTGGCGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA
GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTCATTGATTCACACACCCCCCTCTCC
GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGTCTTCTTCATCAC
AGCCTCATCTACCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTTGCTGACCTAT
GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCTCCACAGG
TTCGTGCTCCTCCGGAGCTGCTCATCCCCCTCTTCGTGCTCTGTAACCTACAGCCCGCGCT
CCAGCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGACTCCTCAGTCTCCCTGTGG
GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTTACCCTCCTGGTGCACCTCATCT**AGA**AAGGGAGGACAAAGGACATTGGT
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACTCGGGCCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCCATGCCCCATTCGTGCAAGGCAGATATTCAGTCTATTTAACAGAACACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
ACATTCACCTTCTTTTAGCCCTTCAAAGATGCTGCCAGTGTCGCCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTTCCAGCT
GACAGCGAGATGCAAGCAATGCTCAGCTCTCCTTACCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCCCTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
CGGGGTGAACAACCTGCCACTAACCAGACTGGAAGAACCCAGAAAGATGGGCTTCCATGAAT
GCTTCATTCAGAGGGACAGAGGGCTCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAGAGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAAA

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FIGURE 48

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGGLQRPEDRFCGTYIIFFSLGI
GSLLPWNFFITAKEYWFMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPMLCLVANFL
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGly
LLLSRLEYARYYMRPVLAHVFSGEEELPQDLSAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTCAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCAGGAAAAGGGCCACTCGCCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCGCGGGAGGGGAACCTGAGC
 CGGCCGGCGGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGTGTCCGGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCCGCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGCAAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTTCGACGCGGCGGCGGACGCTTCGCC
 GGCTTGAGCCGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGGC
 TGTCTGCGCCAGCTCTGGGACGGCACCGGCGTCTGCAAGCGTTGGGCGGAGGACAGCACA
 GCCAGGGTGGCTTTGTGGTACAGCCCGCGCGCTCTGGCAAACCGAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTTGCCGCGGAGCACACCGCCTACCCGCACGGCTGGTGGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
 CCAGTTATCTCTCAAAACAGACCACACAGGAGCTCGCATTAAAGTATTTTCGGA AAAA
 AA

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FIGURE 50

MAPLALHLLVLPILLSLVLASQDQWKAERSQDPFEKCMQDPDYEQLLKVVTVGLNRTLKPQRV
 IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
 HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
 LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEGGFFYLSFAEALR
 AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPFDVHVQIETSPPARNL
 KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG
 HSNTDRPSRMIFYPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQL
 WDGTVVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
 ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
 NTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAAT
GGACCGCTCTGAAGCCACCCCTGTCTCTGGAGGAACACAGCGCAGGGAAGAGCAGGAGCTCTGTTGGCAGGAA
GAATCCAGAGCGGGGAAGCCGCCATTCCTACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCTCT
GCTGCTGTTTACAAAGATGCTTTTATCTTTAACTTTTTGTCTTCCCACTTCGACCCCGCGCTGTATCTGCAT
CTTGACATCTTGGAGCTGCCATCTTTGTGGCTGATCACCAGACCTCAACCCCTCTTACCTCTTCTTGACCTGAA
CATCTAGCTCTGTGGGATTTGAGGGAGGACACGGAAGGGGGTTCCAGAGAACAATGACCTAACAAAGTTGCTG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTCTGACAATGGGCCCTGCTTGGG
ATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC
CTGCTCTCTTGCAATAAAGTTATAAATCATCACCAGACCAGTTTGTGCGGCATCTTTGCTCAGAATAGGCCAGAGTG
GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACTTGGGACCCAGAAGC
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCAAAGGCATTTGGTGCTGAT
AGGGAATGTAGAGAAAGGCTTCAACCCGAGGCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA
GCAAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCAGGCAAGAGCACTTCAG
AAACCTGTGCCTCTAGCCCAAGAGCCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
CACTCTGATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAAGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
CACATTTGTTTCCCGCGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAATGAGGCCAAGACACCCCT
GAAGAAGTTCTTGTTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
TTTCTGGGACAAGCTCATCTTTGCAAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTTGCTACTGGAGC
TGCCCCCATGTCCACTCTCAGTCATGACATTTCTTCCGGGACGCAATGGGATGTATGAAGCTTATGGTCA
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTACGTTGGGGTCCCTCGGC
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAAGGAGAGGCTTCGAT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCTGAGAAGACAGGAGCCCTGGACAGTGATGGCTG
GCTTTCACACAGGAGACATTTGGTTCGCTGCCGTCGCCAATGGAACCTGGAAGATGACCCGTAAGGAGGACTTT
CAAGCTGGCCCAAGGAGAATACATTGCAACAGAGAAGATAGAAAATATCTACACAAGGAGTCAACCACTGTTTACA
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGACTTCCCTC
ATTTGCAAGCCAAAGCTTGGGCTGAAGGGCTCCTTTAGGAACTGTGCCAAACCAAGTTGTAAAGGAAGCCATTT
AGAAGACTTGCAAGAAATTGGGAAGAAAGTGGCCTTAAAACTTTGAAACAGGTCAAAGGACTTTCTTCACTCC
AGAGCCCATTTTCAATTGAAATGGGCTCTTGACACCAACATTGAAAGCAAGCGGAGAGAGCTTTCCAATACTT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCGCGGCCACTG
TGCACTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTTGTTTGCCTTTCCCTCCTATTTTTTTTAAAC
TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAACTTAGTTCCCAATAAATCA
ATCCTGTCTTTCCCATCTTGCATGTTGCTAATATTAAAGCTTCAGGGCTACTTTTATCAACATCGCTGTCTCAA
GATCCAGTTTATGTTCTGTGTCCTTCTCATGATTTTCAAACCTTAATACATATTAGTAACACAGATCTCAAGGT
CAAAGGGACCCCTCTGTGCCTTCTTCTTGTGTTGTGATAAACTAATCTGCCAACAGTCTCTATGCTATTATTA
CTTCACTGTTCAAACCTAAGAGTTTTTAAATCTGAAAACTGCTTCAACTCATGTTTCTTAGCCACCTCCAC
AAACACTAAAAATTTTAGTTTAGCCTATCACCTCATGTCAATCATATCTATGAGACAATGCTCCGATGCTCTCT
TCGCTAAATTAATTTGTGATGACTGAAGGGAAAGTTTGATCATCAAAACATTTCTTAACTCTCTAGTTAGATA
CTGACTTGGGAGTATTAATAATTTGGGTCTATGACATACTGTCAAAGGAATGCTGTTCTTAAAGCATTTATTA
CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTCAGAGTTGCTGCTGAGGCTGTGGGGAGGAGTGCAGA
GGTGGGCCAGTGAACTTTTCAGTAAATGAAGCAAGCACTGAATAAAAACTCTGACTGAGCTGGGAACAAGATCT
ACAGGCAAGCAAGATGCCACACACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCTTGGATT
AGAGTTCTGCTCTACTTACCACAGATAACACATGTTGTTTCTACTTGTAATGTAAGCTTTTAAATAAAC
TATTACAGATAAAAAA

FIGURE 52

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLFTKMLFIEN
FLFSPLPTPALICILTFGAAILWLITRPQPVLPPLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPDAIVHVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCVEHAYEPTPDDVAISYPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADNMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVQLQIFVHGESLRSSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFISIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD
```

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCGGGGGCCCTAAGCCATTCTCGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGTATGAGCACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAATGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGCGGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGCTCCCGCGGGCTCCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACACGGTGTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAAACGTGTGTTTGACACGTACTACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGTCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGGCCTTCGTGGGACGAAAAGAGGTCCTGTCTTCGGGGAGAAACATTC
 TAAGTCACTGCCCTCTCTTCTTGGGGGACCCAGTCTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCGAGTGCCTCTGGGCAGACACAGAGCTGAACCGTCGCGCGCGGCGC
 TTCTGCAGCAAAGTTGAGGCGTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCATCCAGACACAACAGGTCCTCAATGTGCTGTGGCTGTCTATTGAC
 GGAACCCAGCCAAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGCTCT
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGAACCCATGGATGTGGTGCCACT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCATCAGCATCAAGAATGCCCGCTGTCTCAGC
 ACTCAAGGCCAGCCTCACTGCCACTTTCACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGGCTGTGGATTTTTCAGTTTCCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCGCTGGAATGACACAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCCTGTGGAGACCAGTGGCTGGGCTGGGCTGGGCTC
 AGGAGGTCCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTACACCGGAAAAGCTCTGGGA
 TTGGACATGTGGATGCGGATGCCTGAACAACGCGGGGCCGAGAGTGCATCATCCCTGACG
 TTTCCCGATCCTACCACCTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTCACAGAGGCC
 TACTTCAAGAAGCACAGATTCAACACGCTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAAGTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGCAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAAGTGCCTCA
 TATCTGGGACCTGGATGTGCTGAACCAACCTGCGGGCCTGTGGAGATTGTTTTCGGAAGAAGA
 ACCACTCTCTGTGGTGGGGGTCCGGGCTTCCCTCTACTCAGTGAAGAAGCCACCTCAGTC
 ACCCAATTTTCTTGGAGCCACCCCAAGGAGGAGGCCGAGGCCGAGCAACAGAC
 ATGAGACCTCCTCCAGGACCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCTTCATCTGTAGGATTTTGTAGATGTGGTAGGGGCTGGGGCTACCTTGTTTTAACTA
 TGAGACTTAATTACTAATCAAGGGGAGGTTCCCTGCTCCAACACCCGTTCTGTGAGTT
 AAAAGTCTATTTATTTACTCTCTTGTGTGAGAAAGGGCAGGAGAGTACTGGGAATCATTAG
 ATCCTAGCAGCTCATCTCGCCCTTGAATACCTCACTTTCAGGCTGGCTCAGAATCTA
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCTGGAGTTTC
 TTTTGGGCTGGAATGTGCTGCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCTTA
 GACACTGGACAGGCCCTCCTCTCAGCCTTCTCTTGTCCAGATTTCCTAAAGCTGGATAAGTT
 GTTCATTGATTAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLFNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTHAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS
AEEAECHWADTELNRNRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDKNVLNVPVAIAGN
RPNYLRLRLSLLSAQGVSPQMITVFDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPPEAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLVCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLRSYKKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDFTTWTQLAKCLHIWDLVDRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKKEGAPGAPEQT

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAGCCCACTCTCTTGGAACCAACACAC
 CTGTTTAAAGAACCTAAGCACCATTTAAAGCCACTGGAATTTGTGTCTAGTGGTTGTGGTGAATA
 AAGGAGGCGAGAATGGATGATTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATACCTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTGG
 GTGCTGGCCCTTCTCTGTGGAACCTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTCTTGGAGGAAACACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCAGCCACGACCACACACAGTGCATGCCATATATTGGTG
 TTTCCCTCGTTCTGGGCTTCTGTTTCATGTTGCTGGTGGACAGATTGGTAACCTCCCATGTGCATTCT
 ACTGACGATCCGAAGCAGCAAGGTCTAGCAATTCAAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATGT
 TGTTTGTGGCAATCATGCTACATAAGGCACGACTGCTTTGGACTGGTTCTCTTTGATGCATGCT
 GGCCTTAGAGCGGAATCGAATCAGAAAGCCTTGTCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCTCCCTGAGGTGGGCGGA
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGAGGCGCTCAGCCGCCCTGGAAGTGGCAGCCCT
 GGTCTCGGGTGGCCTCATCCCTCTCATCCTGTCACTAGGACACCGAGCATTAATGTTTCAAGGTCCAGC
 TCTGGTCCAGGCCGTTTGGCCATCCAGTCAAGTGAAGAAGCCGCCAGCTACTCACTTCTCTCAGTC
 TCTTGTCTCACTTGGCCATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTTAAACCCCTG
 AGTAATGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT
 TATCTTTTAAAGAGCCCTTGACATTTTGGCTTTTAATATTTCTCTTAACCCCTATTCTCAGGGAAGATG
 GAATTTAGTTTAAAGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTATCCATTGATTTT
 AACATGGTTCACCAATGTAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTTACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGGCTCTCTGAATCCAGCCTGCCATTCCATCAATGCGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTGTCAAGTTCTCCCTTGCAAGAT
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAAAGTTCTAGTAGTTTCAGTTCTTAGGCTTCTCTTCAAGAA
 CAGTCAGATCAGAAAGTGCTTTTGGAAATTAAGGGATATTAAATTTTAAAGTGATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTTTGT
 TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAAGCTTT
 GCGGACACTGTGCTTCTCACATAACCACCTGTAGCAAGATGGATCAATAAGAGAAGTGTTTGGCTTA
 TTGATTTAAAGCTTATTGGAATCATGTCTCTGTCTCTTCTGCTTTTTCTTGGCTTTCTCTAACTTT
 TCCCTCTAGGCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTGTTGTGGGATGAATT
 CTTATCAGGACAACCACTCTCGAAGTGAATAATGAAGATAATAATATCTTTATCTCTTATCCCTTT
 CAAAGAAATTACCTTTGTGCAAAATGCCCTTTGTTGAGCCCTTAAATACCACCTCCCTCATGTGTAA
 ATTGACACAATCACTAATCTGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA
 ATTTTTTTTTCATATTTTGCCAAAATTTTGTAAACCTCTGCTTGCAAAATGAGTGATAATATTGAT
 TATTAATTTTATTTTACTTTCTATACCATTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCAATAGCTAGCATGCCATG
 ATTTATTTCTCTCATGAATTTGTCACTGGATCAGCAGCTGTGAAATTAAGCTTTGTGAGCCCTCTGCT
 GGCCACAGTGGAGAAAGTAGCAAAATAGGATACAGTTGATGTAGTCAATTGGCAACAATTGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAATGACTTCTTGTGATGGATGTTAACAGCT
 GACTGGTGTGAGACTTGGGTTTCTATGTCTCTCAAACATATATGGTTGCCATAGATTCTCTCTGGA
 AACTGCTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAA

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FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQ
IGNSHVHSTDDPEAARSSNSKITTTGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCGGATCCC
 CGAGTGCGCGGCCGGAGCCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAGACCAAGTTAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGAAGGGAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCTAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA
 TAAATGTTTCATGAGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVLDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDRQQQLQALSEPQPRQLQAAGLPHTVEVPQGKGNVLGNSKSQTPAPSSEVVLSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGCAGAAAGCCTCAGTGTGTCTCTTCTGGCCTGGGCTGCTCTCTTCTACGCTGGCATGCCCCTCTTCA
 CCAGTGGCTTCTGCTCACCCTGTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGGCATGGGGAGGCCAAGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGCTGA
 TAGATGCTCTGCGATTTGACTTCGCCACAGCCCCAGCATTACACGCTGCCTAGAGAGCCTCCTGTCTCCCTACCTC
 TCTCGGCAAACTAAGCTCCTTCAGAGGATCCTGGAGATTACAGCCCCACCATGGCCGGCTACCCGATCTCAGG
 TTGACCTCTCTACCACCACCATGACAGCCCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTATTGATGCTG
 GTAGTAACCTTCGCCAGCCAGCCATTGTGGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGGCGGTAG
 TCTTCATGGGAGATGATACCTGGAAGACCTTTTCCTGGTGCTTTCTCCAAAGCTTTCTTCTCCCATCCTTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGGCCA
 AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCTGTGGAGAATTGACACATGCTGGTGTAGTGG
 CTGGGGACCATGGGATGACCACAATGGAGACCATGGAGGGGACAGTGAAGTGGAGGTCTACGTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCAGCACCCACAGAGGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
 CCACGCTGGCCCTGCTGCTGGGCCTGCCATCCCATTTGGGAATATCGGGGAAGTATGGCTGAGCTATTCTCAG
 GGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGGCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TGTCTGAGCTGCAGCATCTCCTCGGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTGTGGTCC
 GCATCGCGGGGGTACTGCTCTTCTGGCTGCTTCTGCTTTATCTGCTCTGGCATCTCAGTGGGCAATATCCC
 CAGGCTTTCCATTTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTGGGGCCTACAGCCTATGCTGAC
 TCTGGGAATATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATCTTCCCTT
 TCTGTGGAAGCCTGGGCTGGCTGGGGGCTCCAGAGGCCCTGGCAACCTGTTCACCATCCCTGGGCCCTGCTC
 GTTACTCCTGCTGTTTTCGCTTGGCTGTGTTCTTCTGTATAGTTTTGTTGTAGCTTCCGCTCAGGGCCACCCCT
 TCCTTTTGGGCTCATTCATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACATAGCTAC
 TCACAATGCCCGCCTTGGCATTGAGCCACAACAAACCCACCGCCAGCAATTTGATGATGCCCTGAGGCTGTGA
 GAATTTGGGTGCTTTTATGTACAAAGCTAGCTGGGCTTTTCATCGTTGCCCTGAAGAGACACCTGTTGGCACT
 CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTCGAGCCAGAATTTAGGTATGGAGCTTGTGTGG
 CGGCGCTGGTGGCCCTGTTAGCTGCCGTGGCCTTGGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCAC
 CCATGCTCTTTGTGCGCTGGGAGTGCCTTAAATGGCATTGGGTACTGCTGCCATGGGCATTGGCGCTCGGGG
 CAGATGAGGCTCCCCCGCTCTCCGGCTCTGGTCTCTGGGCACTCATGGTCTGCCCTCGGGCTGTAGCAGGGC
 TGGCTGCTTCAGGCTCGCGCTGCTCTCTGGAAGCCTGTGACAGTCTGGTGAAGGCTGGGCGAGGCTCCAA
 GGACAGGACTGTCTCACTCCTCTCTCAGGCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
 TCTACCGACACATGCAGGAGGAGTTCCGGGGCGGTTAGAGAGGACCAAACTCAGAGGTCCCCGTGACTGTGGCTG
 CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCAAGCCCTCAGCCTTGGGCTTCCACCTTCTGCTGT
 TGCATCGGAGGATCATGACCTTGTGTTCTGCTCTGTTTTCAGCCATCCATTGGCATGAGCCTTCGTGGGATTCC
 CAGAGGCTCATGGCTCCTGACTTGGCTGCCCTTGTCTAGTGGGAGCCAAACCTTTGGCTCCCCACTCTCTCT
 TTGACTAGGTTGCCACTGCTCTGGCTCTGGCTTCTGTGTGAGATCAAGGGCTGGGGAAGGACAGCAGC
 CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGACGACTGATGGAGATTGCGGCTCGGG
 ATGCGCTCAGCAGCTTATGTGAGCAGCTGCTGAGCTGGGCTCAAGTACCTCTTTATCCTTGGTATTCAAGTAT
 TGGCTGTGGCTTGGCAGCCTCCATCCTTCGACAGGCTCATGCTGTGGAAGTGTTCGCCCTAAGTTCTATAT
 TTGAGGCTGTGGGCTTCAATGTGAGCAGCTGGGACTTCTCTGGCATGCTTGGGTGATGAGTGGATGTG
 CTTGAGCTCTGCTTGGCAGCAGTATTCTTGGCCAGCAGAGGCTAGCTATGCTGATTACTTGGCAGCTTGGCT
 ACAGAGGCTCTGAGAACAGTCTAGCCTGGCCTGTACAGTACTGAGCATCTCAAGCAGGCTCAGCCATAC
 TCTTACTATCATGACAGCAGGGGGCGCTGACATCTAGGACTCATTAATCTATAATTCAAGGACCAAGTGGAGTA
 TGATCCTTAAGCTGATTTGATGCTATGAGGACAAGGGGGCGGTCTCGAAGTGAATTAATAAGGCGG
 GCGTGGTGACTTGCACCTATAATCCAGCACTTTGGGAGGCGAGGTTGGGAGGATGCTTGGTCCAGGAGTCA
 AGACGAGCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAGTGTGAATAAATGATAATAT

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGGKPGACW
MASRFSRVVLVLIDALRFDAQPQSHVPREPPVSLPFLGKLSLQRILEIQPHHARLYRSQ
VDPPTTTMQRKLALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPSPFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGHHPHPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCICLLASQWAISSPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLLFRLA
VFFSDSFVVAERATPFLLGSFILLVVLHWEQQLLPKLLTMPRLGTSATNPPRHNGAY
ALRLGIGILLCTRLAGLFHRCPEETPVCHSSPWLSPPLASVMVGGRKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAVQLGSVYSAMVTALTLLAFLLLLHAERISLVFLLFLQSFL
LLHLAAGIPVTPPGFTVPWQAVSAWALMATQTFYSTGHQVPFAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPPLLLWPFLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFFYAALLQLGLKYLFILGIQILACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAATTTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAAGCTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGT
ACACGTGGAGTCCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAAGAGAAACACCCAGCAAAATTTGATTTTGATTATGGAATGAATTTGACAAAA
GATTCCTTTGGCTGCTGAAAAAATCGTGATTAACCTTATCACCCCTCAATATCTCGGATGAT
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAACAGTCATTGAATATGA
ATATGATGTGAGAACCACTGACATTTGTGCGGGGCCCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCCG
CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTTGGCGCAGGAGCA
CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCTTGGTCGACTGGGATCCCC
AAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCGAG
CCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTATGGAGGAATGGGGGT
TATATGTGCAGATGGA**AACTGAT**GGCAACACTTCCTTTTGCCTTTTGTTTCTGTGCAAAAC
AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
GTTTCATGCATGTAGGTCTCTTAAACATGATGGTGGGCCCTCGAGTCCAGGGGCTGGCCGGT
TGTTCTATGACAGAAAGCAGTCAATAAATGTTGCCAGACTGGGTGCAGAATTTATTCAGG
TGGGTGT

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FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSIQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILIYGNFED
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLDPQAQHTDSEEGPEEEPSTTLVDWD
PQTGRCLCIPSLSSFDQDSEGCPESEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

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FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGGGGCCCCACGTCTGAGTACTGCGGAGCCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGCTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGAGGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCTCTGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCTGGGACCACCAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT
TGCGGCATGCAAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTACGGGTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGCGAGAAGCAAACCCAGTAAATGTTAAGTACAAAAAAGAAA

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FIGURE 64

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGRF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSGDSHRRGFCADS GGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGACAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
CGCCTGTCCCCGGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTGCGGCTGGGCACGGTAG
CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAGTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACCACTGGGTCACTTTCTCTGACAACTTGCTGCTGGAC
AAGTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT
GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGAGACACACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCCCTCCAGATTAACCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCCGCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTCACTTGACAGGCCACGTGAGGAGGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGGACCT
TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACAGAGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGTGTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCC
GAGTTACAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC
TTGCTCATT

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FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop .

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAA YCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGP IFWLLVKSP ELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATGT**GGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTCGGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCTCTGCTTGCATTTACTCTCATCAAACGCGCTGCA
 GTCTGACTGGAGGAATGGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCGCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATATTACCATTGCC
 ATTCCTATGGCTGGAGGAGGCTGTCACTCTTCCGAGGATCTTACGGAGAGTGGAAAGCAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTCACTCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAAGCCCTGGGTTCCCAAGCCCACTCTCTACCAGATCCCAGCCTCTACTGTTCCCTAT
 GAGACCAATTCCAACGCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA
 CCACCGCATTGCTGCCCTCACAGGCCCTTGATGTGCGGCCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCGTCGCTGTTGTTAGGA
 ATGCAGCACTGTTTTGGTGGAAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGCTGCTGTCTGGTGGGAGATAAGTGGGTGGCCAAAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGCCCTGCAGCTCCAGCCCTGAAGAC**TGA**AACCTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAAGAGCCTTGTCACTTTGCTGTGCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACTCTCTGTTGGGAAACAGGACATCTCAACAGTCTCAGGTTCTGCATCAGTGGGT
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCCAAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTAAACACAGTCATTA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAAARGDTFSALTSVARALAPERLLGLRRYLRGEEARL
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTSAITDLYSPKRLFSLTGDDCFQ
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
 LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
 QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
 RSVVASGEKQLQVEYRISKS AWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSSVEAGGATAFIYANLSVPVVRNAALFWW
 NLHRSGEGSDTLHAGCFVLVGDKWVANKWIEYQGFEFRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCTCTGCTCCATCTCAGGAGGCCCTGCTCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGAGCCCCCGTAACCCGCGCGGGGAG
CGCCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTCTACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCCTTCC
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCTCATGTTTCATGGTCTCCTTCATGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
ACTTCTGAACGACAACATTGGAAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCACTGCCCCCTGGACCCCTGGCGCTGTGGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATTCGAC
AAGGAGCGTTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
CTGGTTCATGGACAACATACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCTTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGAGGCACGGG
ATGTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCTCCTTAAGAGGCTTTCCCGAGGCAGCTCTGGAATCTGT
GCCCACCTGGGGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCTGAGGCTCTGCTCAGGGCCCATTTTCATCTTGCCATGTCCTTGCGCGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTTTGCAAGGGCGGCTGCTTCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGATTTTCCCGCATGTCTTATCTTGCCCTTCCCCAACAGTTTGTAA
TCAAACAATAAAACATGTTTTGTTTTGTTTTTAAAAA

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FIGURE 70

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLIISTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGV PYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCCTGGCATCCTGCACCTTGTCTGCCCTCTGA
CACCTGGGAAGATGCGCCGCCGTGGACCTTACCCTTCTCTGTGGTTTGTCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCATGTCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGTGTC
TCAGTGCCATGCGGGAAAAGCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCTGAAGCATCATCTTGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAAGAGCTCTGTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCTTGGTCAAGACCATCGTGAGTTCACATGAGCAGCTAGGCCCAAGCCACCATC
CGCATGGACACCAAGTGCAAAGTGGCCCCACC CGCTGGTCTCAGTGA CTGTGCCACGCCA
TGGGAGCCTGCGCATCCAAC TGTGTATAAGCTCTCCTTCTGGTGAACGCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTTC
CCTCAGCATTTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
AGCTCTACCTGGGGGCCAAGTGTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATTAC
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCCGTTACGCCCTCATCGTGAGTCA
GGACGTGGTGAAGAGCTGCAGTGCCCTGTCTGTGCTCTCCAGAAGAATTATGGTCCCTGTTGG
ACTCTGTGCTTCCCTGAGATGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAGAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCTGAAGAAGTCTTAACTAGGACATCTCCGAGTT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTCTGGAAGTGTTCCTCCCA
GTGAAGCCCTCCGCCCTTTGTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAAC TCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCTATTGGTG
AAGGCCTTGGGATTTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTTGTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGCTGGGTCCCAGCTGGGATATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACCCTGCCCTGTGAAAAA

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FIGURE 72

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNLQCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTWKFNNASAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLT PASLWKPPSPVVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAGAGATGGTGTATTCTGA
 AAAGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCGGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAATGCATAGACAGTGTGTCTGTTGCAAGCAAGCTGATGAAGAAATCCAGATCCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTGGCATGGTGGATTTTG
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATAGAGCCCC
 CAAATTATGCTGGTCCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTCCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTGA
 GCTGAAACACACATTTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTCTTTTATG
 TGAAGCTGTACCTCTGACATGGATATTTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTTCAAGTGATTTAAATAGTTAATCATTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTTT
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCTTGACCAGGTGTTCCACATATGCC
 TGTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTCATCTTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCCCTTTTGTAGTAGAGAAATTATGTGTGTATGTGGTCTTCTGAAATG
 GAACACCATTTCTCAGAGCACAGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTCAGATTCATTCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTAGTGCTAAAATCAGTGAACCTTATACATGGCCTAAAGTTGTTTCTACAAATTAGAGT
 TTGTCACTTATTCATTGTGACTTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGGCAGTGACTTACGCCGTGAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCTGGCCAACATGGTGAACCCCGCTCTCTACTAAAAATAT
 AAAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGGAGACTCCATCTCAAAAAAAAAAAAAA

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FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLEWNTNKRVPVIRMNGDKFR
RLVKAPPRNYSVIVMTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
GAAGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCG**ATG**CTA
CTGCTGTGGGTGTCCGTGGTTCGACGCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCTGTGGACGCTGGACAAAG
GAAGGTTAAACATTTATCCAGGAAGTCAGGTAGTGAACCTTCCTTTTATCAACTTTATGAAG
ACAGTGGGACTTCCCTTCTGAATGCCTACACAACTCTCAAAATTTGTTGCCCATCACGCGC
AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAAATTTAAGGGTCTAG
ATCCAAATTATACAACATGGATGGATGTCTATGGAGAGGCATGGCTACCGAACACAGAAATTT
GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCTGTGGACGCTGGACAAAG
AGATGTTGCTTTCTTACTCAGACAAGAAGGACGGCCCATGGTTAATCTTATCCGTAACAGGA
CTAAAGTCAGAGTGATGGAAGGGATTGGCAGAATACAGACAAGCAGTAACCTGGTTAAGA
AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC
TTACCCCTTCAACATCTTCTGGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTATT
GGCTTGAAAAAGTGTCTCATGTGCCATCAAAATCCCAAAGTGGTCACCTTTGTGAGAAATG
CACCTGTAGATTATTACTCTTCTTATACAAAAAACTGCACTGGAAGATTTACAAAAAAGA
AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGGTTGGTG
AAATTTATTTGGCCCTTCATCAATTAGATCTTCTTTCAGAAAACTATTGTGCATATACTCCTCA
GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG
TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCGCGCCTACAAGTATCAAATG
TGGTTCTCTTGTGGATATTTACCTACCATGCTTGATATTGTGGAATTCCTCTGCCTCAG
AACCTGAGTGGATCACTTTTGTGGCTTATCATCAGAAACATTTAAGAATGAACATAAAGT
CAAAAACCTGCATCCACCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGGCTCCA
CCTACATGCTTCGAACTAACCACTGGAATATATAGCCTATTCCGATGGTGCATCAATATTG
CCTCAACTCTTTGATCTTTCCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAAATTTCC
AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCCTAAGGTTCTG
CTTCTGTCCACCAGTATAATAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGACAGAAAT
TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAAGGAACCAAGGAAGTA
TGAAAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA
GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT
AAATGAACAGTTTTAATAATTACCAAGTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAAGGTCAAGAGATTGAGACCATCTGGC
CAACATGGTGAACCTGTCTCTACTAAAAATCAAAAAATTAGCTGGCGCGGTGGTGGCACA
CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTCGC
AAAAAATAAAAAATAAATAATAAATAATTACCAATTTTTTCATTATTTTGTAAGCAATGTAGTG
TATTTTAAGATAAAATGCCAATGATTATAAAATCAGATATTTTCAAAATGGTTATTATTTTA
GGCCTTTGTACAATTTCTACAATTTTAGTGGAAGTATCAAAAGGATTGAAGCAAAATCTGTGA
ACAGTTATGTTCCCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAAAT
AGTTGTATGTGAGCATTTGATGGTGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

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FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLI RNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENEFGSSTFHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYYSSTYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSVLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSI INYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG
GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAG
TGTGACATCTATAGACCCCTTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
ATCCTTGAGGCCTCCTGGGATTTCATTCTGTGCTGGAATCTTCATGGGATCCTACGGGA
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
GCATTATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
CAGAGAAATCGCTCCAACCTACTACGATGCCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
ATGTGTGAAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGTGTGAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTGCTGCTC
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
ACTGACCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIAQAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPAVNHLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQLATRSPRPGQPPKVKSEFNYSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 79

GCCTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAGGGTGTGAATCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDVFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
 TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
 GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
 GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGA~~AA~~ACTGCACCTTCAGA
 GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGA~~AA~~CTGCGA
 CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGT**CAGCTAA**TGGAACATCAGGGGAA
 CGATGACTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
 TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT
 CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG
 AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
 GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCTT
 TCTGTGAGATTTCCATCATCTCAAGTTCTCTTATCCAGGAGCAAAGCACAGGATCATAA
 TAAATTTATGTACTTTATAAATGAAAA

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FIGURE 82

MAPRGCI VAVFAIFCISRL L CSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDR LCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCGGCACACAGAAGTTCTCTCT
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTGCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCGAGAAGCTCACCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCAGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAGCAAGATGCACCATCCAACCTGTGTGGTGT
 ACCATCCTCCTCCCAGGATAGTGAAGACATCAGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAGAAC
 CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCACGCGGCAGCCTTCTGAGTCTGGGCGCATCTGCTTTCGGAGCCAGCAC
 CCCCCTGTCTCCTCAGGCCCGGAGACGTCTTCTCCCATCCCTGGACCCTGTCCCTGACT
 CTCAAACCTTTGAGGTCACTTAGCCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGTCTGG
 GGCAGGTGCATTTGAGCCAGGCTGGCTCTGTGAGTGGCTCCTTGGCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCAGCCCCCTCAACCCCTC
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTACAGAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCAGGCACACAGGCACAGGTCAGGTC
 GAGAGACTTCTCCCCGTGGCCGCTTGGCTCCCCGTTTGCCCGAGGCTGCTCTTCTGTG
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCTGCCTGCCACTGGCCATCGCC
 ACCTTCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTTGGCAATCTGAGGCCAGGACAG
 ATGTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGTGGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCATCCCCTACTCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAGAACTACATGGGGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLGPDVK
GHDVTFYKTYWRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGCTCTCCATCTCTCCCTCCT
TTCCCCGCGTTCTCTTTCCACCTTTTCTCTTCTCCACCTTAGACCTCCCTTCTGCGCTCC
TTTCTGCCCCACGCTGCTTCTGCGCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
GGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCCGA
CTCCGCTCCCGACAGCGCCTGACCTGGGAAAGCATGGTTCCCGAGGTGAGGTCCTC
TCCTCCTTGTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCC
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCTACT
TGGAGCCACAAGGCCTGATGTACTGCCTGCCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACAAAGTCCTGCC
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
CGCTGCCCCAACCGATGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
AACCTGCCCCGAACAGGCTGCCAGCACCCTCCCACTGCCAGACTCCTGTGTGCCAAGCCT
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
CCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCAAGGGAGCAG
GCAGCACAACGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
AAGACGTAATCCACCGGGGAGGTGTGGCACC CGCCTTCCGTGCCTTCGGGCCCTTGCCCTG
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
ACCCCTGCCGTACCCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAA
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAAGTGTTCCCAAGGCACCGGGCCGGGTCTCT
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
CCTCGGACTTGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCTCAG
AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAAATCTTCCACTTGACTCAGATCAAGA
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
GAAGGTCACTGGAACGTCTTCTAGCCAGACCCTGGAGCTGAAGGTACAGGCCAGTCCAGA
CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLP ERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

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FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

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FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGTYISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVGTTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPTLDTEQ
QWDTPCPRENAEAAAFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPFRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTTCTCTCTAATCCAT
CCGTACCTCTCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
GGGCCAGACAAGCCTGTCCAGGCCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTGTGAGGCTGGAAAACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTT
GATAGAGACATCCAGCTACTCTGTCTAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
GAAAGGTCACAAAGGACAGGATTGTGCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAACCTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA
GAAAAGCTCCCCAGGAGGTGCCCTACTCTGAGAAGAGATTACAAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCATATTAATCCCCGT
TTTATCAGCGCTCTTCCCGAGGACCCACCTACAAAAATAGGGGTCTTCTCGACTATGAGTG
TGGGACCATCTCCTTCTTCAACATAAAATGACCAGTCCCTTATTTATACCTGACATCTCGGT
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAACCTCC
ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCCTCTTGGCAAAGGGCCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCCTTCTCTCCCAGGG
GTGAAATG**TAGG**ATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
GATCCAAAGTCCCGCAGCAGCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
ACATGGGAGTCAAGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATT
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATAACCACTCTCAGGTGAAGAACCG
TCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGATCCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
AAAAAA

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FIGURE 92

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFCFLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSTRNDRMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
 PDHGYWVLRNLNGEHLTYFTLNPRFISVFFRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTSNESSSQATTPFLP
 RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGCGGTGCGGAGGCTTCCTTGGTCGGATTGCA
 ACGAGGAGAAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
 CATGAGGAGCCTGCCGAGCCTGGGCGGCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
 CCGTCGCCTCAGCGCCTCGGCGGGGAATGTACCGGTGGCGGCGGGGCGCGGGGCGAGGTG
 GACGCGTTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTAGGGCGACGGC
 TCCCACGGCCCCAGGCCCGAGGACCGGGCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC
 ACCACCTTTTCAGGCGCGCTCGGCCCCCTCGCCGACCAACCCCTCCGGCGCGGAACGCACTTC
 GACCACCTCTCAGGCGCCGACCAACCGCGCGGACCAACCCCTTCGACGACCACTGGCCCCG
 CGCCGACCAACCCCTGTAGCGACCAACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCC
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCCAACCCACCTGCCACCGAGGCCCTCTC
 TTCGCTCTCTCCAGAGTATGTATGTAAGTCTGCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACGTGTGAAC
 TGCAAGAGGGGCTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAAGCAACAGAGGGTGGAAGTGAAGTTTATT
 TTATTTTAGCAAGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTTACAAATATTTTATATACTTTTATCTCTTACTTTATATGT
 TATATTTAATGTGCAAGGATTTAAAAACATCTAATTTTACTGATTTAGTTCCTCAAAGCACTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATGAAGAAT
 AAATCTGCTTTCTGGAAGGGCTTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAATGTTCTT
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACAGTACATTTTGGAGACCAAAAG
 TAGATTAAGCAGGAATTACTTTAACTATTATGTTATTTGGAGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACGTAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGTGTTCTTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATATAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTATACCTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCAGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCTCTCTACTAAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACCTGTAGTCCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSPLGGLALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSP TTPPAAERTS
TTSQAPTRPAPTTLSTTTGAPPTTPVATTVPAPTTPRTPTPDL PSSSNSSVLTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGCTAGACCTGGGAGG**ATG**GGCGGCCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGGGTGGCTCCCGGGAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCTGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGAC**ATG**CTGCTGCTGCTGCTGCC
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
GGCTGGATTACCCTGGCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
GCACCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCCTGTGTGCCCTGGGCCTGTGAGCAG
GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
CCGCTCCTCGGTGCTCACCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
ATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
GTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTTCAGCCT
CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTTGGGACTCGGGGGGACAGGAGGCCACTGACCCGAGTACTCGGAGATCAAGATCC
ACAGAT**G**AGAAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAGACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
CCACACTGTGCCCTCCCTTTTATTTTAACTAAAAGACAGACAAATTCCTA

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FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDGTGIEDANAVRGASQGFLTEPWAEDSPPDQPPASARSSVGEGELQYA
SLSFQMKVPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

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FIGURE 99

GACGCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCTCTG
GGTGTACACGCTCGGCCTGGCCGCTGCCCTGTCCTTACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCGAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

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FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCGAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGAGGGGAGAGACCAGGATCATCAAGGGGTTGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
GGCAGCGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCGCTACA
TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACAGTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATCTGCCTT
GAAATATTGTGACTCTGGGAATGACAAACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLRCANITIIHQKCEAYPGNITDTM
VCASVQEGGKDCQGDSCGGLVLCNQLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTATTACAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACC GAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTGCTATTTTCCCTATGAGAAGATATTTTGA
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLVGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGVQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFI SPKEYNVYQHDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

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FIGURE 105

CAGAAATGCAGGGACCATGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCATCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACCTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCCTCCCAAATAA
AGTACTTATATTCTC

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FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
GGCTCAGCATCTTTTGTCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGTGTCCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCGTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCCTGCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
CTCCCATGCCA**CCT**GCCATGGTGTGTATCCCGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**
CTGTTTCTCTCCACCTCCACCCCCACCCCTTA**ACT**TGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGA**ACTTCTTGGA**ACTT
TA**ACT**CTCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRFPVRVTSSV
 QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
 AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

CGGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGGAAGCGTTTCGGCTTGCTCAAAGCCCGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCCTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTGGTCATTGAGGGTTTGTGTTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCTGGGGAATCC
TGAGCCTTGGGTCCCTCCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAACCTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGCCTCTTTCGGGTTTCCTTGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
AGGACACAGCCACTCGGGGCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGACGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCCTG
GGTTTGGGGGGAAGGTGACGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAAAGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTGTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFFEKYMEDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGACACCA**ATG**GGCCCCCGGGTGGGCGAGGGTCGGCGCCGCCGTGCGCGCC
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCGCTCCAGCCGTGCGCTTGCCC
CACCAAGTGTACTGCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCGCTCCGCGCGGTTCT
CTCGGGGCATCCCCCGCAACCGTGAAGCGCTTGACCTGGACAGAAATAATATACACGAGTATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCCTCCGAGTCTTGCACTCGGAAGACAACAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTCCAGAGCAGCCCGAAGCTCACCAGACTA
GATTTGAGTGAAAACAGATCCAGGGGATCCCGAGGAAGCGCTTCCGCGGCATCCAGGATGT
GAAGAACCCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCTGGTCAACAGC
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGCAGT
CCACCTGGCCTGGCTCTCGGATTTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGT
TGCCCAAGCCCCCATCTCGGAGCGCCCATCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC
CTGCAGCTGCAGCAATAAATCCTGTCGACTGTGCAGGAAGGGCTTGATGGAGATTCTCGCCA
ACTTGCCGGAGGGCATCGTCGAAATACGCTAGAACAGAACTCCATCAAGAACTCCCTGCA
GGAGCCTTCAACCGACTACAAGAACTGAAGCGAATAGACATCAGCAAGAAATCAGATATCGGA
AGTTCCTTCAGATTGCCCTTCCAGGGCTGAAATCACTCACATCGCTGCTGTCGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTTCGCGAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCATTTGTGTGCGCACTGCCACTTGAAGTGGGCT
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCGAGCAGCCCGCGCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTACAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
TGTGAGGCGACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTACCGACTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGGA
TCTTCAAGAAGTTGCCAACCCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCACT
GGAGACCGTGACCGGCGCGTGTTCCTGGCCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
GTAACTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGGCTGAGTTCGGTGAGACTGCTG
TCCCTCTATGACAATCGGATCAACCCATCACCCCTGGGCGCTTACCACCGTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCACTGCCACTGGCCTGGCTGGGA
AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTTAGGTGCCAGAAGCCATTTTTCTC
AAGGAGATTCCCATCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCGCGCGCTGCCCGGAGCAGTGCACCTGATGGAGACAGTGGTGCGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAAACCACTAACACCGCTGCCAGAGAGCTGTCCGCGCTCCGACACTGACGT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACGGGCTGAGGTGCATCCCGCTCCAGCCTTCAAC
GGGCTGCGGCTCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCTGGAAGG
CTCCTTCAACGACCTACATCTCTTTCCCATCTGGCGCTGGGAAACCAACCCATCCACTGTG
ACTGCAGTCTTCGGTGCTGTGCGAGTGGGTGAAGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAAGGGCCAGTGGACATCAACATTGTGGCCAATGCAATGCTGCTCTCCAGCC
CGTGCAAGAATAACGGGCATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTCGCCCC

TACAGCTACAAGGGCAAGGACTGCACTGTGCCATCAACACCTGCATCTCAGAACCCTGTCA
CTAGGAGGACACTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCTGCCCTCT
TGGGCTTTGAGGGGACGGGTTGTGAGATCAACCAAGTAGCTGTGAGGACAAAGCTGCGAA
AACATGGCCCACTTGCCTGGACGGGATCAACAACCTAGCTGTGTATCTGTCCGCTAACTAC
AAGTGAGCTATGCGACGAGGTGATGACCACTGTGTGCTGAGTGAACCTGTGCAGCATG
AGGCCAAGTGATCTCCCTTGACAAAGGATTCACTGCGAGTGTGTCCCTGGCTACAGCGG
AAGCTCTGTGAGACACAATGATGACTGTGTGCCCAAGTGCCGACGGGGCCAGTG
CGTGGACACAATCAATGGCTACATGCACTTGCCCCAGGGCTTCAGTGGACCTCTGTGTG
AACACCCCCCACTGGTCTCTATGCAAGACGCCCATGCACCAATGAGTACGATGCCAACAG
GGGGCCCAATGCATCGTGGTGACAGAGGACCCCACTGCCCTGCCACCAAGGCTTGCCGG
CCCCAAGCGAGAAGGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAACTGG
CTCCGCAAGGTTCGACCCAGGCCAACACTCCCTGCAGTGGCCATGACAAGGACAAC
GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCAGT
CGCGCTGGTCTATGACAGCCTGAGTTCCCTCAACCAACAGTGTACAGTGTGGACAGCACTGA
ATGATGGGCAAGTTTACAGTGTGGAGCTGGTGACGCTTAACCAAGCACTTGAACCTAGTAGTG
GACAAAGGAAGCTTCAAGAGCCTTGGGGAAGCTCCAGAAGCAGCCAGCATGGGCTCAACAG
CCCCCTCTACCTTGTGGAGCATCCCAACTCCACCGGCTTCGCCCTTGCGCCAGGGCACGG
ACCGGCTCTAGGCGGCTTCCACGGATGCATCCTATGAGTGGCATCAACAACAGAGCTGCAG
GACTTCAAGGCCCTCCCAACAAGTCTCTGGGGGTGTACACAGCGTGAAGTCTGTCCCGGT
GTGAAGACAGCGCTTGTGCGCTTCGTGGAGAAGGACAGGCTGGTGTGCAAGTGCACCCAGT
GCTGGACCGGCCCACTCTGCACAGGAGGCGCGGCAACCTGCCCTCGGCCACAGATGCCAC
CTGTGAANAATGTGTGGAACATGGGACCTATACATGTGCAAGTGTGCCGAGGGCTATGAG
GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCTGTCTGACGCTTCAAGTGTACCATG
GGCAGTGGCCATCTCAGACCAAGGGGAGGCACTACTGCTGTGCCACCGGGCTTTAGCGGT
GAGCACTGCCAACAAGGAATTCGTGCTGGGCAAGTAGTCCGAGAGGTTGATCCGCGCCA
GAAAGGTTATGCATCATGTGCCACAGCTTCAAGGTCGCCATGAAATGCTGTCTGGGGCT
TGGGCCCCAGTGTCTGCGACGCCACCCGCAAGACGCGGAAATACGTTCTCAGTGCACG
GACGGCTCTCGTTTGTAGAAGAGTGGAGAGACACTTAGAGTGGCGCTGCTCGCGTGTTC
CTAAGGCCCTCGCCCGTGCCTGCCACCTCTCGGAATCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCTGGTGTATCAGATGAAAGGAATGAAGCTGGAGAGGAGTTAAAGAGA
AGAGAATATTAAGTATATTGTAAATAAACAAGAAATAGAATTAAGAAATTAAGAAATTA
AAAAAA

FIGURE 112

MAPGWAGVGA AVRRLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRT LR LHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYKKLKRIDISKNI SDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLL NANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHL
 AQNPVFCDCHLKWLADYLDQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEIDYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLP EYVTDLR LNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNDTFAGLSSVRLSLYDNRIITITPGAFTTLVSLSTINLLSNPFCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDL SNNSISMLTNYTFSNM SHLSTLIL
 SYNRLRCIPVHAFNGRLSLRVLT LHGNDISSVPEGSFNDLTSLSHLAGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYGKDCTVPINTCIQNPCHQGCTHLSDSHKDGFSCSCLFGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVP ELNLCQHEAKCIPL
 DKGFSCECPVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPFPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDN DPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWGTPLC
 DQEARDPLGHRCHHGKCVATGTSYMKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQQCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

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FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
 CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
 GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
 CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
 ACAGCTTCGCGTGGTGCAGACGCGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
 GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
 AGTGGA AAAAAGGCTGTGAGGTTTCTAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
 GCCCTAGGATTTGCAGTGAATGTCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
 TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCAT
 TTAAATGTC

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FIGURE 114

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDAIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTCTGGAGCCAGGCCACACCGTCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAACTTTGTACATGGCTCCC
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAAGTGTTC
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG
CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
TTATGACGAGAGAGTCTTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAAATCTCC
CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
ATAGAAAAGTTCATCCGTGAACCTTCTTTAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
AGTGAAGGAAAAATTTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAAATGTCATTTTTATGGATTGTAGACC
CAGTTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAATAAA
CTTGAGTCTTGAATGTGAGCCACTTTCCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
AACCATGTCTTTTATGTCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
TCATTCCATGTTTCAGCAGAGTATTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
TAAATTTTGAATGATGACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCAGATTCAAT
CCACCGAAGTGTTCACTGTCTGTGTAGGGAATTTTGTGTTGCTGCTTTGCTGCGGATC
CATAGCGAGAGTGTCTGTATTTTTTTTAAAGATAATTGTATTTTGCACACTGAGATATAA
TAAAGGTGTTTATCATAAAAA

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FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
 RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
 DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
 HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
 IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKFIREFSLKATMGLAGRARVKEKFSPEAF
 TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAACCACATGAGGAAAAAATTGTATGAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAATCATGGCAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTAC
 TTGATAAAAAACATGACTCGGAAAAAACAAATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTCAAGTCCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAAATTGACCGATTTATTATT
 CCTAGAGAGACCTCGTCCCTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 ATTAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACCTTGTAAATATAAACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
 ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRK
 KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
 DDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIKERKGRNFS
 QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTS EEVQKKLYEEINQVF
 GNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL
 QDPNTWPSPHKFD PDRFDDELVMKTFSSLGFGTQECPELRFAYMVTTVLLSVLVKRLHLLS
 VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

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FIGURE 119

CTAGATTTGTGCGCTTGCAGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCCCGAGGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTCACGTTCAACCCCGAGGAGTATGACAAGCAGGACATTAGCTGG
 TGGCCGCGCTCTCTGTCAACCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
 TCTGCAGTGCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTACCGTCTTTGGGCTGAAA
 AAGAAACCTTCT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCTCCGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
 ATTAATAAAAAAAAAA

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FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

TCCCGGACCTGCCGCCCTGCCACT**ATGT**CCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
 CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
 GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCCTCGTGCCAGC
 AGCAGGCCCCGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCTGGGCTAC
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
 CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
 ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCTGCGGTGTGGCT
 CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
 CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
 ATAAAGATGTAGCTC

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
 AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
 MSIGISFMGNMYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
 IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTTCGTGTTCTCGTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCCAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATCCATAGTGATACCCCTTACTACCCATC
 TGGCT**TGA**CCCGGGGCGAGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTCAGGCAGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGAAGTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGCCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCTGGGGCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTCTTCTGCCAGTACTCCCCCTGTACCACCAATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCAGGGTGGGGCGGGGCCGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGCTGTCTGTGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAATAAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAATGTGCGCGCCGCCGCCGCTCGCTCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCGAGCACCCGGGATCCCGGGTAGGAGGCACGCGGGCGAGCACCAGCGCCAGCC
 GGCTGCGGGCTGCCACACGGCTCACC**ATG**GGCTCCGGGCGCCGGGCGCTGTCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG
 GCGGTGCGGAGACCAACCAGAGCCATCCGAGATGAGCAACAAGACGCGCATATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTCACATTGGAGCTGTCTTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTCAGTTTTACGCGATTAAAGTCTACCAAGGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTCTGGTG
 TTCCCCCT**TAGG**ATTCAATTTCTCCATGATGTTATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAATCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAGAAGACTGTACTG
 TGTAAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGTTCTGTAA
 AAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCCAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAAGAGTCATATTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAATAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGCTTTTGTATAGGTCATATGAATTCATAAAATTTATTTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

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FIGURE 126

MGSGRRALSAVPAVILLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRI IYFDQILVNVGNFFTLESVVFVAPRKGIYSFSF
HVIKQYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

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FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCTATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAAGTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAAACAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 128

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPGTVGIHGDSPPQFFLYSAFMTLVIIILHVFVGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGGCTCGGTGAGAGGCCATCTGGGGGTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG
 AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
 GCRAACAGGACAGAGGGCGTGCCTGTCTGTGAACGCTCTGAACAGCAGAGAGGGGGCGCGTGTCTGTGTGGT
 TCCGCCAGAGAGGGGCTGTGGTGTCTTCCAGGTGCCCTAATCTCGAGGGGATGTTTCAGCGCAAGTACCTCT
 ACCAARAAAGTGAACAGAACCTGTCTGAGCGCCCCACCAAGATGAGTCGGAGATTCAGTTCTCTACGTGGATG
 TGTCACCCCTGTCAACAGTCAACACCAATACCAAGCTCCGGGTCAAGCCGATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTGAGCTTCAATACCAAGCAGCAGCAGCCGAGTACTTCAAGTATGAGTTCCTGAAGGCGTGGACT
 CGGTAAATTTGCAAGGTGACCTCCAACAGGCCCTTCCCTGTCTCAGTCATCTCCATTCAAGGATGTGCTGTCTCTG
 TCTATGACCTGGACAAACAGTAGCCTTATCTGGCATGTACCAAGCATGACCAAGAGGGCGGCATCACCCTGAC
 AGCGCAAGACTTCCCGAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCTCGCGGGGGCT
 CCCTGCCCTTCTACCCCTTTCGCAAGATGAACCGGTGATCAAGGGCACCGCCAGAAACCCCTGTCAAGTGTCTGG
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTCAAGTGGGATGCTCTTTGGCTGGGTATATTTCTCTCCTTTTACC
 TGCTGACCGTCTCTGCCCTGTGGGAGAACTGGAGGCAGAAAGAACCCCTGCTGGTGGCCATTGACCGAG
 CCGTCCCAAGAAAGCGGTCAACCTCGAGTCTGGCTGATTTTCTCGGCAGTTCGCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGGCATGGGGACCTCTCTTACG
 GTTACCAAGGGCCCTCTTTGAACTCTAGGTACTCGGCCGAGTGGACTCCATGAGCTCTGTGAGGAGGATG
 ACTACGACATGTTGACCGCATGATTCGCAAGAAATGTATTCGCAACCAAGATACCTCTTATGTGGCTGACC
 TGGCAGCGAAGGACGAAGCGGTGTTCTGCGGAAAAAGTACCAAGTCTACTTCTGGAACATTTGCCACCTTGTCTGT
 TCTATGCCCTTCTGTGGTGACGCTGGTGATCACTACCAAGCAGGTGGTGAATGTACAGGGAATCAGGACATCT
 GTACTACAACCTTCTCTGCGCCCACTCGGCAATCTCAGCGCTTCTCAGCAACCTCTCAGCAACCTGGGGT
 ACATCTCTCTGGGCTCGCTTTCTGTCTCATCTCTGCAACGGGAGATCAACCAACACGGGGCCCTGTGCGCA
 ATGACCTCTGCTGGATGTGGGATGCCCAAAACACTTGGGCTTTTACGCCATGGGCAGACGCTTGATGA
 TGAGGGGGCTGCTCAGTGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACATCGTTCTCATGT
 ACATGATCGCGGGACTGCTGATCTGAAGCTCTACCAAGCGGCACCGGACATCAAGCCACGCGCTCAAGTG
 CCTACCGCTGCTGCCATTTGTCTCTTCTCTGTCTGGGCGTGGTCTTTGGCAAGGGAACACGGGGCTTCT
 GGATGCTCTTCTCATATTACATCATCGCCACCTGCTCTTCAAGCAGCAGCTCTATTACATGGGCCGGTGA
 AACTGGACTCGGGGATCTTCCGCCGATCTCCACGTGCTCTACACAGATGCTGATCCGCGAGTGACCGGGCGCG
 TCTACGTGGACCGCATGGTGTCTGGTGTGGGCAACGTCACTGGCTGGCTGCCATGGGCTTATCA
 TGGCCCCAATGATTTCGCTTCTACTTGTGGCCATGGCATCTGCAACCTGCTCCTTTACTTGCCTTCTACA
 TCTATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATGCCCTGCTCTGATGATTGGACCTCCGCTGTCT
 GGGGCTTCGCGCTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAACCCCTGCAAGATCGAGGAGACCA
 ACCGGGACTGCATCTCTCGACTTCTTTGACGACCAGACATCTGGCACTTCTCTCTCCATCGCCATGTTTCG
 GGTCTTCTGGTGTGCTGACATGGATGACGACCTGGATACTGTGACCGGGAACAGGATCTATGTTCTTACG
 AGGAGCTGGGCGCTTCGCTTCACTCAAGGGCCCTGAGCTCCTTTGTGTACAGACGACTCTCTGTGCTGT
 GTGGGATGAGTCCCGACCGCTGCCGACATGGATGGCAGCAGGACAGCAGGCTAGCTTAGGCTTGGCT
 GGGACAGCCATGGGGTGGCATGGAACCTTGACGTGCCCTCTGCCAGGAGCAGGCTGCTCCCTGGAACCCCC
 AGATGTTGGCCAAATGCTGCTTTCTTCTCAGTGTGGGGCTTCCATGGGCCCTGTCTCTTGGCTCTCCATT
 TGCTCTTTGCAAGAGGAAGGATGGAAGGGACACCTCCCATTTCTATGCTTGCATTTTGGCGCTCCTCTCCCC
 ACAATGCCAGCTGGGACCTAAGGCTCTTTTCTCCATCTCCCATCCAGGCGCTAGTCTGGGCTCTGA
 ATCTCTGTCTGTATCAGGGCCCACTTCTCTTTGGGCTGTCCCTGGCTGCACTCATGCCATTTCCAGTACGC
 AGGATGGATGGGGTATGAGATTTTGGGGGTGGGCAGCTGGTGCCAGACTTTTGGTGTCAAGGCTGCAAGGGC
 CTGGGGGAGTGGGTATTCTTCTTCTTCCAGCTGTCTGCTGAGCTGGCTTTTGAAGTGGCTCAGCCCAAT
 TGAGAACCGCTCTGATTCAAGAGGCTGAATCAGAGGTCACCTTCTCATCCCATCAGCTCCGAGATGTAGCC
 AGCAGCAGGACTGGAGGGAGAGCGCCTCACCCCTTCCCTTCTTCCAGGCCCTTAGCTTGTGCCAACCC
 AGCTGGTGGCTTTCAAGTCCATGACACTGCCAAGATGTCCAGGGGCAGAGGAGGATGATCAGAGTTCAG
 CCCTGTTCTGCTCCACAGCTGTGGGCACCGAGTGCTACTTACAAAGGGGCTCAGAGAGGCTGTGCTGTT
 CCCTCTAGCTGGCGAGTCTAGCCTCGCTTAGGACCCAGGGCTGGCTTCAAGTTTCGCTCAGCTCTTCAGCA
 AGTTCGTGTGATGATCAGACACATACCTATGAACCTTGAATTTACAAGATTTGCCAGCTCTGGGAC
 CTTGGCCACCTGGTCTTGGATCCCTTCTGCCACCTGTGTCCACCCAGATGTGAGGATGGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGAGGGATGTGTTTCTCCAACTTGTGTTTATAGCTCTGCTGTGAGGGCTGGG
 AGATGAGGTGGGTCTGGATCTTTCTCAGAGGCTCTCCATGCTATGGTGGCATTTCCGTTTTCTATGATGAAT
 TGCATTCATAAACAACAGACTCAAAAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGLVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGEQFSNNTTAAQPQYFKYEFPEGVDSEI
VKVTSNKAFCPSVISIQDVLCPVYDLNNAVFIGMYQTMTKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYFPAEDEPVDQGHRQKTLISVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLISYGYQGRSFEPVGTFRPRVDSMSSVEEDDYDTLTDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLIIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCNPNYTNFQFDTSMFYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLSTQLYMGWRKLDGIFRRILHVLTYDCIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCIILDDFFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCGCTTGCCCCACCCAGCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCCTGTCCTG
 ACCATGTGCTCCCTGCGCTGCGCTGCGCTGCTTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGAGAGCTGTCTGTGGAAAGTTGCAGAAAACTATGGTGGAAATTTCCCTTTATACC
 TGACCAAGTTGCCGCTGCCCGGTGAGGGGGCTGAAGGCCAGATCGTGTGTCAAGGGGACTCA
 GGCAGGCAACTGAGGGCCATTTTGCTATGGATCCAGATTCTGGCTTCCGTGCTGGTGACCAG
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGGCTGAGCCGGGTACCAGGCTGGACCTCCC
 CTTCTCTTCTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGGCCACCAGGCCACTG
 CCACCGTGGAAAGTCTCCATATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAACTCTCAAAGTCTCTATACCCGCACCCACATGGCCCAAGTACAGTGGAGTGGGGGTGATGT
 GCATATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGTGGATGGAGAAC
 TGACAACGTGCCCTATCTGCCCTCCCCGTGACCCACAGTCAGATCCTGTAGCTCAGTGCAC
 CAGTACTGGAAGTGACTAGACTGTGACGAGAGGATGACAGTGCCTCCCGCTCCCCAATTCC
 CACGTTGTGATGCTGCTGACCTGAGCCCTGAGCCTGAGGATGGGCTAGAGGGGAGACCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGGCCAGAAC
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGCGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGGTTTACACTTCCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCGCTTCCGCTCATGGATTGACAGGGGAGACACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCTAGAGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCAGGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGTACGAGGCCAGTGTCCCCATCAGTGGCC
 AGCCGGCTCTTTCTGCTGACTACCATCAGCCCTCCGACCCATCAGCCGAACCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAAATTTCCGGGGAGGTTGCACACC
 GCCCAGTCCCTGCAAGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGGCCAGGA
 TACAGCCCTGACTCTTGTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAGACCAATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGACAGGTCCCTACAG
 TTTACCCCTTGGTCCCAACCCACCGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTT
 CCATGCCTACCTACCTTGTGCCCTGCATTGGGTGGAGCCACGTGGAACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTGCTGCAAC
 GTGGAGGGGCGAGTGCATGCGCAAGGTGGGGCCGATGAAGGGCATGCCACAGAGCTGTCCGC
 AGTGGGCATCCTTGTAGGCACCTGTGATGCAATAGGAATCTTCTCATCTCTATTTCACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCTGAAAGCGG
 ACTGTGTGAATGGCCCCAGGAGCTCTAGCTGGGAGCTTGGCCTTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCAGCAGCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT
 CTGCCCTGGGGTGGAGGCACCATCACCATACCAGGCATGCTCGAGAGCCTGGACACCAAC
 TTTATGAGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTTGCCCAATAATAAGCCCCA
 GAGAAGTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 132

MVPAWLWLLCVSVQALPKAQPaelSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAeyQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGI PFLFLEASDRDEPGTANSDLRFHILSQAPAQPS PDMFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEPAFRlMDFAIERGDTE
GTFGLDWEPEDSGHVRLRLCKNLSYEAAPSHEV VVVVQSVAKLVGPGPGPGATATVTVLVERV
MPPPKLDQESYEASVPISAPAGSFLlTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
QSLGQAQPGDtyTVLVEAQDTALTlAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLTlALHWVEPREHIIPVVVSHNAQMWQLLVRIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGTlVAIGIFlILIFlHWTMSRKKDPDQADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
ATTGAGTCAACTAGTAATTCAAACAACCTGAAGCTCAATTTCTGGAATCTCCCTCCTCCT
TCAATCGGCCCTGTGGATGTCCTGGTCCCATCTGTCACTCTGCAGGCATTTAAATCCTTCTTG
AGATCCCGGGCTTAGAGTACGCACTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGACAGCTTTCTGTGAC
CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAACACCGGCCGATGTATGTACTGAAGTT
CAGCACTGGGAAAGGCGTGAGGCGGCCGCCGCTTTGGCTGAATGCAGGCATCCATTTCCCGAG
AGTGGATCTCCCGAGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAAGAG
GATCCAGCTATCACTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC
TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACCGGGTCCCGAAATC
CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTTTGCAGGAAAG
GGAGCCAGCGACAACCCCTTGCTCCGAAGTGATCCATGGACCCACGCGCAATTCCGGAAGTGGA
GGTGAATCAGTGGTAGATTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCTGCTCAAAAGGCCACAGATGCC
GAGGAACTCGACAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGCAATCTGTGTGCGGCACCTGA
GTACCAAGTGGGTCCCACCTGCACCACTGCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
CGTATGACAAACGGCATCAAAATTTGCATTACATTTGAGTTAGGATACCCGGACCTATGGC
TTCTCCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGGATGGCTCTGCTCTGTCTACATTTAT
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTTCCCTACCTGTGTGAG
TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCAGCTCCCTGGAGT
CGTGTGTCCTGGCGGTGTCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTCT
CTGTTTTTGTGAGCCCTTTTGTCTGTTTCTCCTTCCACCTGCTGGCTGGGGCTGCACTC
AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC
TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
GTGGGAGACCACTTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTTAATTTCT
TCGAGCTTCCCTGGAAAAATATTTTCTTTGAGCAGCAAACTCTGTAGGATATCAGTGAAG
GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGTAGACAGAGTTTTGCTCTTGTGGC
CAGGCTGAGGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA
ATTTCTCTGCCTCAGCTCTTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCAGTGA
ATTTTGTGTTTTTGTAGTAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA
ACCTCAGGTGATCTGCCCTCCTTGGCTCCAGAGTGGTGGGATTACAGGTGTGGAGCAGCTG
TGCCGGGGCCCTCCCTCCTTTTTTGTAGGCTGAATACAAAGTAGAAGATCACTTTCCCTCAC
TGCTGTGAGAAATTTCTAGATACTACAGTCTTACTCCTCTCTTCCCTTTGTTATTCAAGTGT
ACCAGGATGGCGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGCTGGGTGAA
GTGACCATCTAAATTTGAGGATGGTGAATTTATCCCCATCTGTCTTAATGGGCTTACCTCCT
CTTTGCCCTTTGAACTCACTTCAAAGATCTAGGCCTCATCTTACAGGCTCTTAATCACTCAT
CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT
TCTTTGCTCCTGGTTTGT
TCTGTCTATTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAAATCATCAACCACT
GCCTCCTGTTTCAATTTCACTCAGCACGTACCATCTGTCTTTGTTGTTGTGTGTGTGTGT
TTGTTTTTGTGTTTTTGTGTTTTTCAACCAATCTGTGTAATCTTAACCTCCTGCTAGGATTTGTACA
GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

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FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLLWRKTRSRNPGS
SCIGADPNRRWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDNL

Signal peptide:
amino acids 1-16

[illegible]

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FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSTANTGSSVISSGASTATNSGSSVTSSGVSTATI
 SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
 SNGAGTATNSESSTTSSGASTATNSDSSVTSSGASTATNSESSTTSSGASTATNSESSTSS
 GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTSSEAST
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAGLFFAGLFFCVRNLSLRNTFNTAVYHHPGLNHGLGP
 GPGGNHGHAPHRPRWSPNWFRRRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATGC**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCCAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGTCTGGGAGAATAATGTGCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGGTGGGGGTGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

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FIGURE 140

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTKELDKGVQGLNHGMDKVAHEINHIGGAGKEAEKLGHVNNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 141

CTCCGGTCCCCAGGGGCTGCGCGGGCCGGCTTGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCGCGGGGGCGGATACCGTGCCTGACCTGACTCACTCCAGTCCGAGGCGGGGGCCCCCGGGGCGACTCG
GGGGCGGACCGCGGGCGGAGCTGCGGCCGTGAGTCGCGCCGAGCCACTGAGCCCGAGCCCGGGGACACCGTCT
GCTCTGCTCTCCGAATGCTGCGGACCGCGATGGGCTGAGGAGCTGGCTGCCGCCCATGGGGCGCGTGGCG
CCTCGGCGACCGCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCGAGCGCGCTCCGACTCGGGCGCTCAGC
CCCCGATCAGCGCTGCTGCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGCAAGTGAACACATCTCCAACATAC
ACAGCCCTTCTGCTGACAGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTTTTGTGCACTCAGTAGC
AACTTCAGCTTCTGCGCAGGCGGGAGTACCAGGAGCTGCTTTGGGGTGCGAGACGAGAGAAGAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGGACTGTCAAAACTACATCAAGATCCTCTGCGCGCTCAGCGGAGTCAC
GTGTTCACTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGGAACCTTCACCTGGCAAGG
GACGAGAAGGGGAATGTCTCTGGAAGATGGCAAGGCCGCTTGCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTGTATGGCGAGCTTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCGCCACCAAGACCGAGAGCTCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCTCAGCTTAC
ATTCTGAGAGCCTGGGCGAGCTTGAAGGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTTGTGTCGCCATTCGCCGATCTGCAAGGGCGATGAGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCAGCGCCGACGATGGCTTCCCTTCAAC
GTGCTGACGATGTCTTACGCTGAGCCCGACGCCCGAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT
TCCGATGGCACAGGGGAACACAGAAGGCTCTGCGCTCTGTCTTCACAATGAAGGATGTGACGAGAGTCTTC
AGCGGCTCTACAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCCAACCCCGG
CTGGAAGCGTGATACCAACAGCTGACCGGGGAAAGAGATCAACTCACTCCCTGAGCTGCCAGACCGCGTGTCT
AACTTCTCAAGGACCACTTCTGATGACGGGAGTCCGAGCCGATGCTGTGCTGAGAGCCAGGCTGCG
TACCAGCGCGTGGCTGTACACCGCTCCTGGCTGCACCAACCTACGATGTCTCTTCCTGGGCGACTGGTGAC
GGCGGCTCCACAAGGCGAGTGAGCGTGGGCCCGGGTGACATCATTTAGGAGAGTGCAGATCTTCTCATCGGGA
CAGCCCGTGCAAGATCTGCTCTGGACACCCACAGGGGCTGCTGTATGCGGCTCACACTCGGCGGTAGTCCAG
GTGCGCATGGCAACTGACCGCTGTACCGGAGCTGTGGGGAGTGCCTCTCGCCCGGGACCCCTACTGTGCTGG
AGCGCTCCAGCTGCAAGCAGCTGACGCTCTACAGCGCTCAGTGGCCACGAGGCGTGGATCCAGGACATCGAG
GGAGCCAGCGCAACGACCTTTGCGAGCGTCTTCGGTTGTGTCGCCGTCTTTGTACCAAGTAGGAGAGGCCA
TGTGAGCAAGTCCAGTTTCAGGCCAACACAGTGAACACTTTGGCTGCGCGCTCTCTCCAACTGGCGACCCGA
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCCTCGGCTCCTGCCAGTGTGCAACCTGGGACCTGCTGCTG
GTGGGACCCCAACAGCTGGGGGAGTTCTCAGTGTGGTCACTAGAGGAGGCTTCCAGAGCTGGTAGCCAGTCA
TGCCACAGGTTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATATCAGCACA
TCGCTGTGTAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGACAGACGGTCTCTGGAAGGAGTTCTGGTG
ATGTGCAGCTCTTTGTGCTGGCGTGTCTGCTCCAGTTTATTTCTTGCTCTACGGGACCGGAACAGCATGAAA
GTCTCTCTGAAGCAGGGGAATGTGCCAGCTGCAACCCCAAGACTGCCCTGTGGTGTGCTGCCCTGAGACCGCTC
CCACTCAACGCCCTAGGGGCCCTAGCACCCCGCTCGATACCGAGGGTACAGTCCCTGTGACAGACAGCCCGG
GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGTCTCGTGGAGGTATCCCCAGT
TGCCGCCGCGCGGGTGCCTGCTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACG
TGCCCTTGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCACTGGACCTCCCTCGCTGCTGCTCTCTGTGGAAC
ACGAGCTGGTGGCCCGGCTTGGGAGCCTTGAGGACGCTGGCTGCTGCTCCAGTCAAGTAGGAGAGGACTCC
TACCACCCAGACCCCAACACCGCTGGGCCAGAGGTCCTGGCCAAATGGGGGCTCGCTAGTGTGGTGAAC
CAGTGTCTCTATGTAAACTGAGCCCTTTGTTTAAAAAACAATTCGCAATGTAGAAATGAGGAGGAGAG
ATGATGAGTGGATCGAGCACACCGCTGCTCCAGTTTCATGGCTCCAGAGGGTGTGGGATGCATCAAAAGTGG
TTGTCTGAGACAGATGTGAACACCTACCAACTGGCTCTTCACTTCCGATTAATCCCGCTGCCACGGCTGCT
CTGTGCTCACTGAGATCAGGACAGCTGGGCTGCGTGGTGTCTGCTTCCGAGTACCGGAGGATGTAGTGTG
TTGTGCGCTGCTGCTCACTCAGGACGAGGCTAGGTTGGCACTGCGGCTCAGGCTTCAAGGATCTGAGGCTG
GGACCACTCTGGACCTTCCAGCCTGTATCAGGCTGAGGACGAGGACGAGGACGCGGCTCAGGAGGA
TTTCTGTGAATGTACGCTTCTTCTCAAGATTCAGGGAAGAGACTGCGCTTCTCTCTGTTGTGGTGA
GAACCCGTGCGCCCTTCCCAACATACACCTCGCTCCATCTTGAATCAACACGAGGAACATCACTGACC
CTGGTCTCTCCCGACCTCCCACTTCACTTCCCTCAGCTTCCCTCAGCTTCAAGGATATCAACACTGCC
AGCACAGGGGCCCTGAATTTATGTGGTTTTATACATTTTTTATAAGATGCACTTTATGTCATTTTTATAAA
GTCTGAGAATTACTGTTTAAAAA

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FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFS PMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFGQNDPAISRSQSLRPPTKESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKLKHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP
QLATRPWIQDIEGASAKDLCSASSVVSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIISTRSVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECASVHPKTCFVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRRVRVLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGCGCGCGCGCGGCTACGAAGAGGACGGGACAGGCGCGGTGCGAACCGA
GCCACGCCAGCCGAGGACCGCGGACAGGCGGGGACGGGAGCCCGGACTCGTCTGCCCGCGCGCTGTCGCCCGTCG
TGCCCGCCCGCGTCCCGCGCGGAGCGGAGGAGCGCGCCACCTCGCGCCGAGCGCGCGCTAGCGCGCGCG
CGGCTCATGTCCTCTTTAAAGCGCAGCGCGCGCGCGCGCGGCTGTGCGGAACAAAGCGCGCGCGCGCGG
CTGTCGGCGCGGCTCGCGGCGCGGATGGCGCGCGCGCGCGCTGCGCGCGCGCGCGCTGCGCGCGCGCGCGCT
CGCGCTCATAGGCGCGGCTGGCCTCCGTGGCGGGGGACAGCGGCTGAGGCGCGCGCGAGCTGCGCGCGCGCGCG
GGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC
TGCTCGGCGCTCGTCTGGGCTCTGTCGTGGCTCGCGGCTCGTCTGCCCGCGGCTCCGAGCTGAAGCGAGCGG
GCCACGCGCGCGCGCGAGCCCGAGGGCTGCGGTCGCGGCGAGCGCGCGGCTCCGAGCGCGCGCGCGCGCG
CGCATCGCGCGCGCGCGCAGCTCTGGCGCGCGGCTCGGACCCAGATGGCGCGCGCGCGCGAGCACTTCTCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCGCGCTACGAACCATGGTCCAAAGCAA
TTCTGGGAAAGTTCAGTCTTCTCAAGTAGGGGTTCTGACACATCTGTACCAATTCAGTAGTGCACTACGGG
GTGTGGACGACTCTACCGCGCCAGAGAAGTCTTTCATGATGCTCAAGTACATGACAGCACTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAGGAGACCGTCTGGAGAACTCTCGAGGAGTT
TGAACAGCAGCGAGGCCCTCTTCTTGGGCAGACAGGCTGGGCACACGGGAAGAAATGGGAAACTGGCCCTGG
AGCCTGGTGAGAACTCTGCATGGGGGGCGCTGGCGTGTATGAGCGCGGAGGTTGCTTCGGAGAATGGTGCCG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATCGCGGAGCTTTTATGAGAATACGAGCAGCAAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAAAATCACCAAGCTATCACATTACACCCCAACAAAACCCCTACCAAT
ACAGGCTCCACAGCTACATGCTGAGCGCGAAGATATCCGAGCTCGCCACTCGCAACATACAGCTGACCGCGGAAA
TTGTCTGATGAGCAAAATACGCAACAGAAATCATAAAGAGGACCTCCAGCGAATCCCTCCCTCCTTCA
TGAGGTTTCAAGCCCGCGCAGAGAGGAGATTTGGAATGGGAGTTTCTGACTGGAAATATCTGTATCGGCGAG
CTGACGCCAGCCCCCTGAGAGGAATGGACTCGGCCAGAGGGAAGCTTGACGCAATGTCTCATGAGCTCA
TGGAGATGATCAATGCCAACGCCAGACGAGAGGGCGCATTTGACTTCAAAGAGATCAGTAGCGGCTACCGCC
GGGTGAACCCATGTATGGGGCTGATGAGTACCTCTGGAACCTGCTGCTTCAAAAAGCACAAGGGAAGAAA
TGACGTCCTGTGAGGAGCGACGCGTATTACAGCAGACTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAAG
TGGATGCACAAGAGTTGGCCAAGAGAAATCAATCAGGAATCTGGATCTGTCTTCTCTCAAACTCCCTGAAGA
AGCTCGTCCCTTTCACTCCCTGGGTGGAAGAGTGAGCACAAGAAGCCAAAGATAAAAAGATAAACATCAATGA
TTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTATGGGAAACTTTGAGAAGAGCTGTCTATTCCCAAT
AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATCTGACTCAACCCCTGACAAGGCGCAACAGTTGAAGTATGA
GAGATTACCGCATTAAGTACCCCTAAGGCCGACATGCAGATTCTGCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
CCCTGGAAGTAGGATCTCCAGTTTAAACATGAATCTTTGCTCTTCTCTGGGAGCTGCAGCTCGTGTATTACTA
CAGAATTCCTTCAGCAGATGTCGAGCAAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCAGT
ATGACCCAAAGATGTTTATAGTCGGAAGTTCAGAGTGACAACCAATTTTGGCTTTACTCAGAAAATGGCTCTT
GGAGAACTATGGGTTTGGCATCAGGTATTTATAAGGGAGATCTGTGCGGAGGTTGTGATGTTTCCCA
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAGGTTTCCAGGAGTTTGAAGAGCTTTAGGAGCC
AGGAAGTAGGAGTAGTCCAGCTCCAGCTCTGCTTTTGTGATCCCAATTTGACCCCAACCAAGTACAAAATGT
GCTTGGGGTCCAAAGCATCGACCTATGGGTCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAATATGATCAA
GTTACAGTAAAGCAGCAATAATAATGGCTCAGTAGGACAGGCTTAATGTCAGCTTTGCTGGAAAAGAGCTTTT
TAATTTATCTAATTTATTTTCAAAAATTTTGTATGATCAGTTTGTGAAGTCGATATCAAGGATATATTTTCA
AAGTGTTTCTTACATAGGACTCTTTAAGATTGAGCTTTCTGAACAAGAGGCTGATCAGTGTGCTCTTGAA
CACATCTTCTGCTGAACATTTATGAGCAGACCTGCTTAACCTTGACCTGAAATGTACCTGATGCAACAACTTT
TTTAAAAAATGTTTCTTTTGGAGCCCTTGCTCCAGCTCTGAGCAGAAACGTGAACATTCCTCAAGATAT
TATTTGTAACAAACACTGTAACTCTGGTAAATGTTCTGTTGATTTGAACATTCACAGATCTTACCTTTTGT
GTTTGTGTTTATTTTACAAATGTTTAAAGCCATTCATGTTCCAGTGTAGATAGAGAAATGTGATAATA
CGTGTTTCATCATGTTCTTCAGGAGAGCTTTCAGAGTTGATCATTTTCCCTCATGTTGATCTGCTCAGCATGGC
CAGTAGGTTTGTGTTGTTTGTGTTTGTGTTTGTGATCCCAATTTGAGACGGAGTCTCACTCTGTACCCAGCGTGAAT
CAGTGGCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTTCAAGCAATCCCTGCTTTGCTCCCGAGT
AGCTGGGATTACAGGCACACACCCAGCCCAAGTATGTTTGTGATTTAGTAGAGCGGGGTTTCCAGAT
GCAAGAGGCTGGCCAGCTAGGTTTAAAGCAAGGGCGTGAAGAAAGCAACGTGAGGATGTGCTCTGCTCTCG
TGATGCTTCATTGGCTTAAATAGACCTGGCATTAATTTCAAGAGGATTTGGCATTTCTCTCTGACCTT
CTCTTTAAAGGGTAAAAATTAATGTTTGAATGACAAGATGAATTTACATAAATCTGATGTACAGCAT
GAACATACACACATACCCCTAAATCAAAACGTGGGGAATAATGTTTGGTTTGTCTCTCATCTGTCGTCG
TGTATTGTTGGTGGAGATGGTTTCACTCTTCAATCTGTTTGTGTTTGTATCTGAAATAGCTTTAA
TTTATTTAGGATCTGTTGTCAGAGCTTCGCATTTCTTGAGACTGTTAGTTAGTATTTATGTGATCTCGG
GAGTGTGTTTGTGCTGTTTATTTGTCAGTAAACCGATCTCCAAGATTTCCTTTGGAACGCTTTTCCCTCG

FIGURE 143B

TTAATTTTATATTCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACAGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAAATTAAACACGAAAAAA

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FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop .
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE
ILEWEFLTGKLYLSAVDQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKPEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSPDNHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCGLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTAAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCTTACAGGAGGCTTACACCGGAAATAGGAAAGAAAAACACACGGAAGTACCCC
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAACAACATGTATAAGTCCAGTTATTGCCA
 GTAGACGAACAAGTAATAAAATTTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTC
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTGCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTATTAACAATAATATAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
 TTTAAGCAAACTGCATTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
 AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGTTTCAGGAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFFTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEEPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDILKKILDINSVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQQLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCTGCTGTCTCTGTTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATGG**GCTTTTGTGCTCATTTTGGTTCTCAGTTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCTGAGACCAAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGGAACTGAGTTTGTGAAGGACTCCATTGACAGGGGGGCGTGCTCTCTAAGGC
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAAGTCCAGATTTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCCTCATTTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGATGGGGATGATAATGTTTCTTCAAATCCAAAGGAAAAATCCA
 GGCGGAAGTGGACTGGAGAAGAAAGCAGGACAGGCAGAAATTGAGAGACGCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTAAGTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACAAATGTG
 ACTTTGTCTCCCAACAATTTGGGTATTGGGTCTCAGACTGACAACAGAATTTGTATTTTAC
 ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCAAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCAGATGATACGA
 GGAAAGGGGACATCCCATATTCATATGTCAGTGTCTGGGGAT**AG**AGACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACACCCAGACCCAGACACAGCCAAGGAGAGATGCTCCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCAAGCCCCCATCTCCTTTAGGGAGC
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGAGTCAAGCTTCCAGATGAGGGGGGAT
 TGGCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGCTAGTACCGGACAGTGATTCTCGCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGGTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTATTCCACATTAATTTACTTTTTCTCTA
 TACCAAAATCCCATGGAAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAAATAAGAG
 GAGGTAGGATTTTCTAGTATTCTATAAGCCAGCATTACCTGTATACCAAACAGGCCAAAG
 AAAACGAGAAGAAGGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTAAACAAATTAACATAAACAAATATTTAAAGAGTATATATAACTACT
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAAGTGTAAAT
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop .

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAA
 TTACTATAGCACATTGTCATTTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGA AAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAATTA AAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCACTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGAGTGCTGCTCACTGTTTACAAACATATAA
 GAACCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATGTCCATGAAAATACAAACCCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGAGCTACAACCT
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AGAGACAAAAGCCTCATGGAAACAGATAACATTTTTTTTGTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCTCTGTGAGCAATAGTTGAAACCTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTTCATTTGTTCTCTAGAAGTTTTGTGCAATTTTGAC
 TTGTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTCAAGCAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTTGGCAGAGAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTTCATTATGAAAGGTCAAGCAAAAGACAGCAGAAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAAACTTCATGCAATGTACTGTTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTMSQRLESMVKNIFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPYPTNAVHRVCLPDASYEFQPGDV
MEVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAAGCTTCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCCGGCTGTCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGACGCCCTTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**
AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGAGTCATGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTCTCGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGG
 CCCAGCGCGGACGATCGCTGCGCTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTCTTCTGCTTGGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGGCTGTTTCCCTTATCAT
 TGTGGGGATGTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGTCTGTGCTTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGTGGCTTACTCATGCTTGGAAATTTTTTCAGAGAGAGTTTAACT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTAGAGAATCCCAGGATGTTCCAAACAGGCCCCACCAGGAAGATCTCAGTGA
 CTTTATCAAGAGGTTTGTGGGAAGAAAATGTATTCCTTTTGGAGGAACCAAACTGAG
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCTGGGACAGACCAAAATGATGTC
 CTTGAAGAATGACAACCTCTCAGCACCTGTCTATGCTCCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTATAAAAAGAAATGTACAGAAAGAAAACCAAACTGTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATTGTGTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAAATAACA
 CTTAAGCATATACTATTCTGCTTTAAAAATGAGGATGAAAAAGTTTCATGTCTAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCGAGCATGGTTTGTATTAGCATTTTC
 CGCATCCATGCAACGAGTACACATATGGTGGGACTGGAGCCATAGTAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACATAATA
 ACTTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAAATATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTAAAA
 TCTGTATAAATTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATATGAAAAGGAAA
 ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCTGTAAATAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGGAAATTA
 CCAGTGTGATACATAGGAATCATTATTACAGAAATGAGTCTGGTCTTTAGGAAGTATTAATAA
 GAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGATGCTGTTTTCTCCCAAAATG
 AAGACTCTTTTGCACACTAAACACTTTTTAAAAAGCTTATCTTTGCTTCTCCAAACAGAA
 GCAATAGTCTCCAAGTCAATATAAATCTCAGAAAATAGTGTCTTTTTCTCCAGAAAAAT
 GCTTGAGAGATCATTAAAAACATGTGCAATTTAGAGATTCTTTGTTTATTTTCACGTGATTA
 ATATACTGTGGCAAAATACACAGATTAAATTTTTCACAGAGTATAGTATATTTATTT
 GAAATGGGAAAAGTGCAATTTACTGTATTTTGTGATTTTGTGTTATTTCTCAGAAATATGGAA
 AGAAAAATAAAAATGTGTCATAAATATTTTCTAGAGAGTAA

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FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTILTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCCTGCCC
TGCACCTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
CCTGTGTGGGGAGGCCCTCCTGCTGCCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
ACCGGGAGGATCACAGAGCCAGC**CATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
CTCGATGTCAAACCCCTGCGCAAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
CCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG
TGATTCTGGATAAAATACTACTTCTCCTCTCGGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
CCCCGAAGGGCCTCGAGTGGCAGTCCGCCTCTCCAAGGACCGATCCCACTGACAGGTGCTGG
ACTCGGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
TGTTGTGAAATCACAGAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTC
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT
GTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGCCCTTGGCAGGTGAGCATCCAGTACGA
CAAACAGCAGCTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCAGCCCACT
GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTACTTTCTCAGGCACAGTCAGGC
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGA
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
CTGATGTACCAATCTGACCAAGTCGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
GGGCCCCAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGACGTGCTGGGAGCGCTTCCTTCTCTG
CCCTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
CTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCTCAATTCTCTGTAAGAGACCC
TCGACGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
GGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAAGCCAGATCACTGTGGG
CTGGAGAGGAGAAGGAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA
CTAGAGCAAGAAACAGTTGTAATATAAAATGCACCTGCCCTACTGTTGGTATGACTACCGTT
ACCTACTGTTGTCATTGTATTACAGCTATGGCCACTATTATTAAGAGCTGTGTAACATCT
CTGGCAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQLDVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSIIDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

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FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGACAGCGGCATCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
 TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGGAGGGGCCATGCCCA
 GGGTCAGATACTGACAGGGATGAACCTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCCTCAGGATTTTGACA
 CTCTGCTCTAGTGGTGAGAAATACCTCTACGTGGGGGCTCGAAGACCATTCGGCCTTGATATCCAGG
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
 AGAAGAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAAATGACCCATCTCTACA
 CCTGGCGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCATCTCGG
 AGGACAAGGCTCATGGAGGAAAGCCAAAGCCCGCCCTTTGACCCGCTGACCAAGCATACGGCTGTGTTGGTGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCACTGAGCCCATCTGATGCGCACACTGGGATCCCAGC
 CTGTCTCAAGACCGACAACCTTCCTCCGTGGCTGCATCATGACGCTCCTTTGTGGCAGGCATCCCTTCGACCC
 AGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACATCGCGGTGG
 CTAGAGCTTGCAAGAACTGACGTGGGCGGCGAAAGCTGCTGCAGAAGAGTGGACCACTTCTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGCGAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCGATTCTCCCA
 CAGCTCCCCACATCTACGCACTCTTCACTCCCACTGGCAGGTTGGCGGGACACAGAGCTCTGCGGTTTGTGCCT
 TCTCTCTCTTGAGCAATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAGAAACTTCAAGCTGGACCTA
 CTTATAGAGGCTCTGAGACCACTCCCGGCCAGGCAGTTGCTCAGTGGCCGCTCCTCTGATGAAGCCCTGACCT
 TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGTGGGACGCCCCCTGCTGGTGAATCTGGCGTGAAGTATA
 CACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACACCACAG
 GGTGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGAAGAGATTACAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGACGTGGGCCCCCAACCCAGGCTGAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGA
 GGGTGCCCGAGCCAACGTAGTGCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCACTGTGCTCT
 GGGACCTGAGTCCGAACCTGTGCTCTGCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCGCAAAATCATTAA
 AAGAAGTCTCGGCTGTCCCAACTCCACTCTGGAGCTCCCTGCCCCACCTGTACAGCCTTGGCCCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATGTAGGAG
 ATGGAGTTGGGGGTCTTACCAGTGTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
 ACAGCCAGGACCAGACCTGGCCCTGGATCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
 CCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTCACTGTCACTGTCTCTCT
 TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTGGCTCCCCATGTAGAGCACTCCGGGTCCGGGCAAGG
 TTCAGGCTGTGAGACCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
 AATGCAAGACCTCTGCCAGTGATGTGGACCTGACAACAACCTGCCTAGGCATGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGGCTGCGGTGAGGCACCTGGCCATGCTGGCTGGGCGGCCAAGCAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTGTGAGCACTGATGACCTCAGAGGAGTG
 ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCAGATGAGCTCTCTAACAGGGTGGGGCTAC
 CCCAGACCTGCTCCTACATGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTC
 CAGAAACACAGTGTTTCAAGAGACCTTAAAAACCTGCCTGTCCAGGACCCCTATGGTAATGAACACCAAAACATC
 TAAACAATCATATGCTAACATGCCACTCTGGAAACTCCACTGGAAGCTGGCGCTTTGGACACCAACACTCCCT
 TCTCCAGGGTCATGAGGGATCTGCTCCCTCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTC
 TTTCTGAAGTCTGACCACCTTTCTTCTTGTCTCAGTTGGGCGAGACTCTGATCCCTTCTGCCCTGGCAGATGG
 CAGGGGTAATCTGAGCCTTCTTACTCCTTTACCCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTTGT
 TTTGGGATTCAAAAACTGCTGTGACAGACTGTTATTTTATTAATAATATAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSSLGLFLFQLQLLLPTTTAGGGGQGPMRVRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAIPSTQVVYFFFE
ETASEFDFFERLHTRSARVCKNDVGGKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTGSLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPPLTRVSGGAALAAQQSYWP
HFVTVTVLFLVLSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVEDADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAAG
 TGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCCACATGCTTAAACCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAGAGAAATTAAAAAGAGTTTGGATTCTTTCTGGGAAGAACTTTAGG
 TGGCAGAGGAAAAATTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTTCCGTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTTCCACTTCATTGGCTCTTTTGGAAATTTGGGCTACCAATCCCCTTGTCTTATGTTCT
 CAGTATCCGTTTCTTGTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACTCTGACTTTGGCTTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT
 GTTGAGGCTTGATGGA AAAACCTATTAAACCAAGTACCACAAGACTTGGGAACCTTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACTCTGCAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCA GTTCTCATTGGCCCCAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGTGGA
 CTGGCTTCTCAGAGTGACCTCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCG
 GGCAGAAATAGCAATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAAGCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTTCTATTACAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCGAGTGGCTGCCAGTGTCTCCTGCGCTCCCAACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGGCCATA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGCGACGTTTTTGTGTTTCTGCTGGGGC
 TCAC TCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCGAGCTTGGCGGGGCTGTTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTCTTGGCAGCCCCATTCTCTAGTCCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAATCATCCTTCCACTTGC
 TAA TTTTGTGTACAAATTATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTTCCAGTCTCT
 CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCATGACCCTCAGATTTCAGCCTTAAATCCACCTTCCTTCTCATGCGCCCTCCGAA
 TCACACCCGTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACCTTGCATATCTTTCAGTTTCTGTTTT
 TGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTACAGGC
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT
 CTTGGCTGACGAGCATGGAGACTGTAGGTTCCAGATTCTCTGAAAATAAAAGTTTACAA
 CGTTATCTCTCCCAACCTCACTAA

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FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKGRP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCFFLIAEKLGPFFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELEWF
INSDFAFDFAFARPLLPNTVYVGGLEMEKPIKPVPODLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIVKWCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLGLLT
LGTWLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGCGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACATACCATGTT
 CTCCATCCCCCAGGTCAGCCCTCAGTGTCTCCCATCCAGCAGGGCTACCTCGAAGCTCT
 GGCTGCAGGCCCTCCCGTCCAGTGGGCGAGGGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACATGCATGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGGCGGGCTGAGAAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
 AGACGGGGGCACCTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTCTTCTGGCCCTGGGGGCC
 GGGTGGGGCCAGGAGGGGTGAGAGCCCGTCTCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA
 CCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCAATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCCGTGCCGGGGTGTCTACAGTTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCAAACCTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCCTTGA
 CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCCGGGGAATCTACTGGTGGTTGGAATACT
 CAAGTTTCTCTGGCTTCTCTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAGAAT
 CCAGCCCCGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTTCATGGGACCTTGTGCCAAACACCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCCAACCCCAAGTTTACC
 CTCCCAGCCACCTGCTGCATCTGTTCCCTGCTGAGCCCTTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCATCTTTTGGCGCCTCTGCTCCTCCGGTTCCCCCAACCCAGCTTCTCT
 GCTCAATGCTGATCAGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCTGACAGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCCTCAGAAGCTGAGCCAGCACCSTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAGGGGTGTATTG
 TCTAGACTGAACATGGTACACATTTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTGCCACCTGAGATTAG
 GGTGAGTGTGTTTCTCTGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTCTGCTTGGCACCTCTGAACTGCTCCAC
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCTCCTCTCTCTCCAGCTCTC
 TCACCTGAGTTATCTTCACTGTACCTGTTCACGATATCCCCACATATCTCTTCTCTCTGAT
 CTGTGCTGTCTTATCTCTCTCTTAGGCTTCTTATACCTGGGATTCCATGATTCTATCTCTT
 CAGACCCCTCTCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTCTTATCCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGCAAGATGCCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAAATTAATAA

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FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

[illegible]

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FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIHAVLYFTWLVDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMSSGGICPVSRTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

GGCGGCGGGGATGGGGGCGGGGGCGCGGGCGCCGCACTGCTGAGGCCCCGACGAGGGCCGGCCGGGCCA
GGCGCCAGGAGCGCGCGCGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGAGCGCCCGCGGACGAGCAGGTGGCG
CGCGCTGCTGACGGCTGTCCAGCGCGGAAGCCGTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCTTGGGA
GCGGTGCTCTACGGAAGGGCGGTGACCCCGCTCTGAGCAGCACTAGGGCTGCTGGCTCTGTGAAGACCTCA
GTTCTGTCTGCACCTGCTGGTCGGCTTGTCTTCGTGGTGAGTGGTCTGTTATCACTTCTGCTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCGCCTCAACTGCCGCTCGCTTACTACTCTGGAGCCA
ACTGTGTCATGCTGCTGGAGTGTGTCTCTGCACGGAGTGATACATGTTACGAGCAGGCCAGCGTAGAGAGTGTGA
TGGGAAGGAGCAGCAGCTATCATCTCAACCAACTCTGCAGATCGACTTCTCTGTGGGTGGACCATGCTGTGA
GCGCTTCGAGGTGCTGGGAGCTCAAGGTCTTCGCTAAGAAGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAAC
GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGACACCGTGGTGAAGGGCTGAG
GCGCTGTGCGGACTACCCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTACGGAAGACCAAGCA
CCGCTTAGCATGAGAGTGGCGGCTCTGAAGGGCTTCTGTCTCAAGTACCACCTGCTGCCCGGACCAAGGG
CTCTACCACCCGAGCTCAAGTGGCTCTGGGGGAGCAGTCGACGTGTCTATGATTAACCTCTCAGAGAA
CAAGAACCCTCCCTCTGCGGGATCCTCTACGGGAGAAGTACGAGCGGACATGTGCGTGAAGAGATTCTCT
GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACAGGAGAAGGACGCGCTCCA
GGAGATATATATACTAGAAGGGCATGTTTCAGGAGGACAGTTAAGCTGTCCCGGAGGCGGTGACACCTCTGAA
CTCTCTGCTCGGCCACCAATTCCTCTGCTCCCTCTTCAGTGTTTGCTCTGGGCGTCTTGGCAGGGATCAC
TTCCTGTATCTGACTTCTCTGGGGTTGTGGGAGAGGCTCCTTTGAGTTGCGCAGATAGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGCGATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAACAATAAACCCAGAAATTCTGGAGTTGAAGCTGTGATTTACTGACATGAAAA
ATTCATAGAGGCTGAACAGCAGATTGTGAGCAGGCAAGAAAAAATCAGCAAGCTTGAAGATGTAGACTTGAAGATT
TTTCAGGCTAATGAAAAAAGATGAAGGAAATTAACAGCTCAGAGACCACTGGTGACCCGTACACAAATCAA
CATATGCATGATGAGAGTCCGAAGAGAGGAGGAGAAGGGTCAGAAAGATGGCCACAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAAGCTCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCAT
AATCAAAGTGTCAAATGACAAAGAAATCTTGAAGAGCAAGAGATGAGCAACTATCTTGTTCAAAGGATCTTTG
ATCAGATTAAACAGCTATTTCCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGTTGA
AACCTTCAAAGTGAATTTCTTCTTTGAGTCTTAGATGTGCTCAGTCTTGTGCTCTCAGGAGGAGTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGAAGCTAGGAGAGGCTGTCTTTAGGCCGGGACAGTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCGCCAGACGGGTGATCATTTGGGGTCAGGCTGATCTCAAACCTCT
GAGTTCAAGGTGATCGCCGCTCAGGCTCCCAAAGTGTGTGATTTGACAGCGCTGAGCCACTGCGCTGCGCCGA
ATTCTTTTAAAGCTGAATGCTGGGGGCGAGGCACGATGAGCTCAGCGCTGTGATCCCAAGTAGCTTTGGATTGA
AACATGCACCACATCGCTGCTCAATTTTGTATTTTATGAGAGACGTGTGATGCGAGGCTGGTCTGATCTCCT
GACCTCAAGTGACCACCTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTTGGCTTGA
GCATTTTGTGATGTGCTTATGGGCATTGTGATATCTTCTATCTTTTGGGGAATGCTGTGTAAGTCCCTTTG
CCTTTTAAATTTTATTTATTTATTTATTTATTTTATTTGAGACAGGGTCTGTGTTCTGTGCCAGGCTGGAGTA
CAGTGGCAGCTGAGTTGTGCTCAGCTGCATCTCCAGCTGGAACAGAGTGAAGCTGCTTCT
AGCTGTATTTTGTATTTTGTATTTTGTAGCTGTAGTTTGTATTTTGTGAGAGACGATTTTACCATTGA
TGCCAGGCTGGTCTTGAACCTGTAGCTCAAGTGATCTGCTTCTCAGCCTCCCAAAGTGTGGGATTACAGA
CATGAGCCACTGCACTGSCAACTCCCAAATTAACACACACACAAAAACCACCTGATTCAAATGGGCA
GAGGGGCGGGTGTGGCCCAACTACAGGGAGACTGAAGTGGGAGGACTGCTTGGGCACTGAGAAGTCAAGGCTG
CAGTGAGTCAAGGTTGTGCTCAGCTGCATCTCCAGCTGGAACAGAGTGAAGCTGCTTCT

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FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop .
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVSVSGLVINQVQLCTLALWVPVSKQLYRRRLNCRLAYSLWSQLV
MLEWWSCTECTLFDTQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAACTGAAGTACTATGCATCACTCCCTCCAATGTCTTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGACCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTTCTCTTGTCTCGTTCTGTAAGTGGTATGCCATGGGGTCTTTCACAAGCCT
 TTCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCGAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCGAAGTGGCCAGCTCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCATACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCCTGATTCAGTAGGCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

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FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRHIHL CVCF SFALALGHFL LISLVGKGLSLSCGVGGRQAGLR LIRPWVRR
EGKINFY TNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCFP GQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
ATTAATACTGTGTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCAAACCTGACCTTCACCTCTGGAACGAGAAGAGAGGTTTCTACCCAC
ACCGTCCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTA
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATGACAAGCCCGAAGATT
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCAGCTGCCCGCCCAT
CTAACCTTTTCAATGCTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAG
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCAGAAGGGCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCAATTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
GGGAAGGAACTTGTGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAAGGC
ATCGAGTCTCCTGCATTCAAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGACGCCGTCTGGGAAGGAGCAAGCAAAGTGACATTTCTCCTCCCTCCTTCCCTC
TGAGAGGGCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGCCCTTATACCCAGGAGACTTGTATTGAATTTGAAACCCCAA
TCCAACCTAAGAACCAGGTGCATTAAAGATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
GTGTGCCGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

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FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCTCCTGCCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTTGGGGAGGCGGT
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCAACC
TGGCGCGGCTCATCCAGGCC**AAGA**AGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCCGCGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGTGCGACCCGGAGGCATCCTCGCCGCTCCTCAGAGTCTGTGGCGCGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAAACGCATCCGGCGG
GACGTACGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTTAAATTGGAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLPPEDSRLWQYLLSR
MREHPALRSRLRLTLEQPGQDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

[illegible]

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FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGNKRGKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSDDQDFTPEKKAARAPRRGRLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVSKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRREARRRELEARRRREQEELRRLREQEKEEKERRRERADRGAEARGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSARKPQSSSTE'PARKPGQKEKRV
RPEEKQQAQKPVKVERTKRKSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALLEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGELAGEEAPQEKAEADKPKSTDLAPVNGEATSQKGESAEDEKEH
EGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

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FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
 ACACCACTTTGAAAGAGACATCTTTTTCATC**ATGAAT**GCTAATAAGAGTAAAAGACTTAAAGCCAGAGGCCAAGA
 TTTTCACTTTTCTCCTGTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGACACTTTGAAGCA
 AATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAATAGCTGTATTCCCTTTTTGGGTTTCATC
 AGAAGGACTGGATTTTCAAACCTCTCTCTTAGATGAGGAAAGAGGCGGCTGCTCTTGGAGCCAAAGACCACAT
 CTTTCTACTCAGTCTGTTGACTTAAACAAAAATTTTAAAGAAGATTTATTTGGCCTGCTGCAAGGAACGGGTGGA
 ATTATTAATTTAGCTGGGAAAGTGGCAATACAGAATGTGCAAAATTCATCAGAGTACTTCAGCCCTATAACCAA
 AACTCACATATATGTGTGGAACTGGAGCATTTCATCCAATATGTGGGTATATGTACTTTGGAGTCTACAAGGA
 GGTATTTATATTCAAACAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAGAGATGTCGATT
 CACTCGATCCCTTGGGCCCTACTCATGACCACCACATACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTTATGGAACCTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTCTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAACGACGCTGATAAAACAAGTGGAGCAGCTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
 TGAATGGGCGAGATACTTACTTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTTAAATGGTCCATATGCTCATAAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGGAAT
 TCCTTATCCACGGCTGCTGATGCTTCAAAGCAAAACCTATGACCCACTGATTAAGTCCACCAGAGATTTCCAGA
 TGTGTCATCAGTTTCTATAAAGCGGCACCTCTGTGATGTATAAGTCCGATTAACCGATTGCGAGGAGCAACAGTT
 CAAGAGAAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCTTTCAAGAGAGTGGCCAGTACGA
 TGTAAATGTTTCTTGGAAACAGACATTGGAACCTGCTCAAGTGTTCAGCATTTGCGGAGAAAGTGGAAATATGGA
 AGAGGTAGTGGTGGAGGAGTTGCAGATATCAAGCACTCATCAATCATCTTGAACATGGAATGTCTCTGAAGCA
 GCACAAATGTACATTTGGTTCCCGAGATGGATTAGTTAGCTCTCTTGCACAGATGCGGACACTTATGGGAAAGC
 TTGCGCAGACTGTTGTCTTGCACAGAGACCCCTACTGTGCTGGGATGGAATAGCATGTCTTCGATATGCTCTTAC
 TTCTAAAAGGAGAGCTAGACGCGCAAGATGTAAATATGGCGACCNAATCAACCAGTGTCTGGGACATCGAAGACG
 CATTAGTCTATGAACTGCTGATGAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
 TAAATCCCAACAAGCAACTATTAATGGTATATCAGAGGTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAAGAGAGGATTCTGGGATGATTTACTG
 CAAAGCCACGAGGACACTTTCACTCACACCATAGTGAAGCTGACTTTGAATGTCAATTGAGAATGAACAGATGGA
 AATATCCCAAGGGCGAGAGATGAGGAGGGGACAGGTCAAGGATCTATTGCTGAGTCACGGTTGAGATACAAGA
 CTACATCCAAATCTTTAGCAGGCCAAACTTCAGCCTCGACAGTACTGCGAAGCAGATGTGGCACAGGGAGAAGCG
 GAGACAGAGAAACAGGGGGGCCAAAGTGGAAACACATGCAGGAATGAAGAGAAACGAAATCGGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACG**TAGT**TTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC
 TATAAAACATATGCTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCATGGAGTTTGTCTAAGG
 CACAAGAATAATCTGAATAAGAATAATGTGATGAATAAAGAAAGGCAAAATCAATTTGAACAGCTTTT
 CCAAGAACAAATCTTGCAACAGCAAATATAAGAAATATCCTTAAAAATAGGGGGTTACAGTTTGTAATGTTTTA
 TGTTTTGAATTTTGAATTTTATTGTACTATAATAGTTAGCTAAGCAAGCCGAATTTGATAGTGATAAGGT
 GCTTTTATCCCTCGAATGTCCATTAAGCATGGAATTTACCATGACAGTTGTGCTATGTCTTATGAACAGATATAT
 CATTCTTATTTGAAACAGCACTACCTTTGGTAGGGAATAAGAGGTGCAGACACAATTAAGACACATCCCATATTC
 AACAGGAATCTTCTCAGTGAGCCATTCTACTCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATATTTCTTCT
 TGGCCACTGGGTTTAAATTTAGTGTACTACCAATGATTTACTGAGGCACTAATGTTTCCCCAGGATTTCT
 ATTGACTCTCAGAGATTAACAGGTGCAGAGAGAAGTTGGTGCTTAGTATGTGTTTTTAAAGTATATACTAA
 GCTACAGGGACAGATGCTTAATAAATACTTTAATAAGATATGGGAATAATTTAATAAACAAGGAATA
 TATGATGTATTAATGCTCTGATGGGAAGGCATGCAGATGGGATTTGTTAGBAGACAGAGGAAGAAGCAGCAT
 AATTTCTGCTTTTGGGAAACATCATATCCCATGAAAGGAAGAACAATCAACAAATAAGTGAGATTAATGTA
 TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAAATTCATCTTTTAAAAAAATTCAGATATTAACA
 AACTGCTAGCAAAATCTGAGGAACAATAAATCTTCTGAGAAATCATGGAAGATAGACATTTTATTTATAACC
 AATGATATTTTCAGTATATTTTCTCTCTTTTAAAAAATATTATCATACTCTGATATATTATTTCTTTTACTGC
 CTTTATTTCTCCTGTATATTTGGATTTTGTGATTATTTGAGTGAATAGGGAACAATAATATACACAGCA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTTGTGAATACAGAACAGATGTAAATTTTAAAC
 AACGGAAGGGTTAAATTTAACTCTTTGACATCTTCACTCAACCTTTCTTCACTTGCCTGAGTAACTCTGTGTAAT
 GTAGTATCTTTTGTAAATTTAAATAAATAGGCTGCTACATGT

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FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYKDLLSNSCI PFL
GSSEGLDFQTL LLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVLCCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRLGPTHDDHYIRTDISEHYWLNCAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTI LSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRI PYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSII LNMELSLKQQLYIGSRDGLVQLSLHRCDTYGKACADCCCLARDPYCAWDGNA
CSRYAPTSKRARRRQDVKYGDPITQCWDIEDSISHETADEKVI FIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLT LN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRRNRHRDLDELPRAVAT
```

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACTGAGCTGGAAGCCGACAGAGTTCATCTGGAGCATGCCACCAGCGGGGAGCAGA
CAACCTCCACAGGTAAAGCTGGGAGCAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTTCAGCCAGCAGGGACTGATCAGGTGTGTGCTCTGGAGTGGGGAGCAGAGGCGGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCAT
GGGTGAGGTGGGGGGGACAGGTGTCAATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGGTGCTGATGAGCTACAGAGGGGAGGGAAAGGTATTTTAAAGTTAAACAGTGTGGCACAATAGTTAA
GAGCAGAGTTTGTGAGCTAGACCAGACATAGGTTCAAATTCCTTCTGTTGCTTCTTAGTTCTTAGCCCCAGGT
AAGGAGTGACTTAACTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAAATAATAGCACCCACCTCAT
AGGGAAGATTAATGACATAATGTATGTGATGCACTAGCAAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACACAGGTAAGTCAACAGCTGGAGCAGAGGCGGACGAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGGACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGACAGGGGGCTGGCTTAGATGTGGAGGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCGCCAGGATGAGGTGGAGCAGAGCGCGGCTCAGTGAGGCTCGGCTGTGCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCCGCTTGGCCACAGGGGCCCTCCCTGCCCTGCACACGTGGTATTTCCGTATCAGGACGGGCTGAGGATG
AGCTGACAATCAGGAGGGTGAGTGGCTGAGGCTCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCAGCGGCGAGGTAGGCTTTGTCCTGAGCGATATCTCAATTCGCCGACCTTCCCTCCAGAGAGCAGCC
AAGCAGTGACAACTCCGCTGCGGGCAGAGCCACAGCATTTCTGGCACAGGCCCTGTACAGCTACACGCCAGAGA
GTGCAGAGTCAAGCTGAGTTCCTCGAGGGGCACTCATCCGTCTGCTGCCGGGCCCAAGATGGAGTAGATGAGC
GCTTTCTGAGGGGAGAAATTTGGGGCCGCTGTTGGGGTCTTCCCTCCCTGCTGGTGGAGAGCTGCTTGGCCCCC
CAGGGCCGCTGAAGCTCTTGACCTTGAAACAGATGCTGCCCTCCCTTCTCTCTCCACGCTTCTCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCTTGCACCTGTCTGCTGGGCAAAAGCCCTGGACTTCCCTGGGTTCTCTGG
ACATGAGGCGACCTTCAGCTCAGGCCGATGCTGCCACCTTCCCGCGGGCTAAAGCCCGGATCTGGCCACCT
CAGATCCCTCACCCTGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGTCCTTATCTTCAAGCTGTGAGGA
CCACACCATCAATGATCAGGACCAACAGCAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCCTTGGGGCTGGAAAC
GGAACTTGCCTTCCCTTCTAGAGCTGGAACCCATCCTTTTTCCTATGTTCTCATCTCTAGGACC
ATCCATCAAGGTCTCTAGTAGTTCTTGGCCCACTCTTTCCCAACCTTGGCTCCATGACCCACCCACTCTGGATG
CCAGGCTCACTGGGGTTGGCTTGGGAGAGGAAACAGGCTTGGGAATCAGAGAGCTGAGGAGTGGCAAGCAG
CTGTAATGTTGAGGCGAATTTATGACAATGAATAAAGGGCAGCAGGGCCAGGCGCAGGGCTTGGGCTTTGTG
CTAAGAGGGCAGGGGCTACCGTGCTATTGCTTTAGGGGCCACACGGGCGAGGCGCTGCTCCAGCTGCCAC
GCTCTATCATATGAGAGCGGTGTTGGGGAAGCGGGGAGGCAAGCTGTTGACAGCAGGGGAAGGAGAAGAGAC
TGAGGGCTGTGACCTCTGCTGAGGCCCACTGAGCTGTGCACTCCAGGTGGAAGTAGAGCTGTGTCCTC
AGCTGGGGGGCAGTGCTGTCCAGTTGAGGGGAGGGGCTTTCAGGCCCAACCCACCTTGGCCCTGCGAGCTGGTAT
TCCATCAGCACAAATGAGGAGCTTGGAGAAGAGGAAGAATAACAGTGTCTCTCTGTTCAAGGCTGTGTCAGC
TTTTCCCTTGGGGCTCAGGAGACTTCCCTACCTCCACCACCAAGGATTTATAGCAAGGGTCAAGCTGCTC
AGTTTACTCTGGGGTTTCAAGGAGCCAAAGGCTTAAATAGTTTAAAGTAGTGGGAAGTAGAGATTACCTCA
TTTAGGGCTCAGGACAGCTCACTCATATCTCCCTGCTCCCTGTGTTAGAGACACCTTGAGAGAAGGGAGGGG
TCAACAATGAGAACACAGGAGTAGGCTCTATCAGTGCCCCCAGAGTAGAGACATAAGAGCCAGCCAGCTGCG
AGTCCGGCTGTGTTTCTTACTCTGGTATCAGAGTGTCTGGTGTGCTTGGCTGCCATTTGCCCTTGTGATGG
CGAGCCTGGGCTGGGCCCTTCCCTGCGGCCCTCAGTGTGGCTGTGCAAGTCTTGGGGTTCCCTTCAAGT
CAGAGGGGGTAGGCTGCTGCTGAGTCTCCATCTGTGACTGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
CTCAGGGGCGAGGCTCTGCTGAGGAGCATCCTGCTGCTTGGGCTGCCCTGCCAGACCCCTGACACCCCTG
GGTCTGTGCCACCAAGGCCCAAGCTCTGCTGTGCTGGGGGAGCCATACGGGTGTCTGTGATCTCATAGGCT
TCTCAATTTCTTCAACCCGAACTTGGGAGGGAGGGAACATGGGTTTACGACCAACTCAGAGGCTGCTGTG
GCCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGGGCTTCTC
AGATTGGGGCAGCTTGTGAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAGGCCACTT
TTGGGATCAGTGCTGATCACTGGGCCCTTACCTCAGCCCTTTCCTTGGAGCACTGCCCACTGCCCACTGCCA
CAGGAACACAGTGGTCTCCCTGTCCGGGGCGGCTTTTCTTCTTGGAGCTCCCTGACGAGCAAGTGGAG
GCCTCTTGTCTGCGCTCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGAGGGGGCT
CGTCTGACGGCTGGAGTCACTCCACTGACAGGAGGAGGAGTGGGATTAACATTTCCATTCCCT
TCATGTTTGTCTTCTACGTTCTTTCAAGTGTCTTCAAGCATGCTCTTAAACCCAGAGGCGAATTTCCCAAGCCCATTT
TTCTGTGCTTATCTAATAACTCAATATTAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCPLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPSSQSDSNPCGAEP TAF LAQALYSYTGQS AEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFP SLLVEELLGPPGPP ELS DPEQMLPSPSPPS
FSPPAPT SVLDGPPAPVLP GDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHDPDLT
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FIGURE 179A

CACAGGGAGACCCACAGACATATGCACGAGAGAGACAGAGGAGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAGGCACAGACAGCGGCAGGCACAGAAGCGGCCACAGACAGTCTACAGAGGGAGAGGCCACAGAAAGCTGCAGA
AGACACAGGCAGGAGAGACAAAGATCCAGGAAAGAGGGCTCAGGAGGAGAGTTTGAGAGAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAAACGGTCTCAGCCCTCTCGAAACTTTGGC
TCTGACCTTTGGCAGGAGTCCAGGCCCCAGGCTACAGAGAGGAGCTTCCAAAGCTAGGGTGTGGAGGACTTTGGT
GCCCTAGACGGCCCTCAGCTCCCTCCAGCTGCATACCACTGCCATGCTCCAGAGCTTGTGCGCCTTGCA
CTTGGCAGGGCGCTGGCTGTGGGAGGCCAACCTGCCTCCTGCTCCCACTGTGCGCCTCTCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCGGCTGGCCAGCCCTCTCCCGGGAGGAGGAGAT
CGTGTTCACAGAGAAGCTCAACGGCAGCGTCTTGCTGGCTCGGGCGCCCTGCCAGGCTGTTGTGCGCCTTGCA
GGCTTTTGGGAGAGCGTCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGAGGGGCTGACAGTGCGAT
CCTGGGCCAGGCGCTGAGACTGTGGGTGGAGCAGAGCCTGGCACTACTGCTGGACCATCAATGAGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAAATATCGGGGGGCTGAACTCCA
CCTCCAGCCCTGGAGGGAGGCCACCCCTAACTCTGCTGGGGACCTGGGGCTCACATCTACGCCGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGACCCCGAAGGCCAA
GGCTTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCACCGGTGC
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCGCAGGCTTCAAGCACCCCAAGCATCCGCAATCC
TGTGAGCTTGGTGGTCACTCGGCTAGTGATCCTGGGGTCAGGCAGGAGGGGGCCCCAAGTGGGGCCAGTGCTGC
CCAGACCTGCGCAGCTTCTGTGCTGCGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CAGCCATTTCTGTTACCGCTCAGGACCTGTGTGGAGTCTCACTTGGCAGCCTGGGTATGGCTGATGTGGG
CACCGTCTGTGACCCGGCTCGAGCTGTGCCATTTGTGGAGGATGATGGGCTCCAGTCAAGCTTCACTGTGCTCA
TGAATGGGTGATGCTTTCAACTGCTCCATGACAACTCCAAGCCTGCACTGATTTGAATGGGCTTTGAGCACA
CTCTCGCCATCTCATGGCCCCGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCT
CATCACTGACTTCTGACCAATGGCTATGGGCACTGTCTTAGACAACACGAGGCTTCATTTGATGCTGCTGTG
GACTTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTGGGGCCGACTCAGCCCATTTGTCC
ACAGCTGCTGCTGGCTGTGCTGGCTGTGGTCTGTGGCACTCAATGGCCATGATGGCCATGATGGCCACCA
CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCGCACAGGCTGCATGGTGGTGGTGGCTCCCATGTGAGCA
GCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGCTCCTTGGGAGCATGGGCTGATGCTCTCGGACTGT
TGGGGTGGTGTCAAGTTCTCTCCGAGACTGCACGAGGCTGTCCCGGAAATGGTGGCAAGTCTGCTGAGG
CGCGCTAGCCGCTTCGCTTCTGCAAACTGAGGACTGCCAACTGGCTCAAGCTGGCTCAAGCTTCCGAGGAGCA
GTGTGCTGCTACAACACCGCACCGCACTCTCAAGAGCTTCCAGGGGCCATGGACTGGGTCTCTGCTACAC
AGGCGTGGCCCCCAGGACCACTGCAAACTCACTGCCAGGCCGGGCACTGGGCTACTATATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTTCGCCGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCATGTCTG
CTGTGATCGCATCATTTGGCTCCAAGAAGAAGTTTGACAAGTGATGGTGTGCGGAGGGGACGGTTTGGTTCGAG
CAAGCAGTCAGGCTCCTTCAGGAAATCAGGTACGGATACAACAATGTGGTCACTATCCCCCGGGGGGCCACCA
CATTTCTGTCCGGCAGGAGAAACCTTGGCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCTTGGGCGACTCAGCTTGGCTCA
CAGCGGGGCACTGCAGCTTCAAGAGACACTGTCAAGCATGGGCCACTGGCCAGCCCTTTGACACTGCAAGTCT
AGTGGCTGGCAACCCCGACACACCGCTCGGATACAGCTTCTTGTGCGCCGCGGACCCCTTCAACGCCAGC
CCCCACTCCCAGGACTGGCTGCACCGAAGAGCAAGATTTGAGATCTCTCGGCGGCCCTCGGGCGGCGAG
GAAATAACTCACTATCCGGCTGCCCTTCTGGGCACCGGGGCTCGGACTTACTGCTGGGAGAAAGAGAGGCTT
CTGTGCTGCTCATGTAAAGTCACTGGGGAGGGGCTGTGGGCTGAGACCTGCCCTCTCTGTGCCCTTAAT
GCGCAGGCTGAGCTTGCCTTGTTCTTCTGCCCTGGGAGGCACTGATGGTGTAGTGGTGAAGAGGGCTGACAGC
AGCCCTCATCTAACTGCCCTTCTGCCCTGCGGTCACAGGAGGAGGGGAGGGGCGCTGGGCC
CAGTTGTATTTATTTAGTATTTATTTCACTTTTATTTAGCACCGGGAAGGGGACAGGACTAGGCTCTGGGGAA
CTGACCCCTCAACCTCATAGCCCTCACTGCCCTGAGGAGTCCAGGCTGGTGTGATGATGATGATGATGGT
TGTGATGCGTGTGTGTGTGTGTGGAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTCTGCTTTCCCT
TTCTGAAATTTTATTTTGGGAAAGAAAGATCAAGGTAGGGTGGGCTCAGGAGTGAAGGATATCTTTT
TTTTTTTCTTCTTCTTCTTTCTTTTCTTTTGTGAGACAGAACTCGCTCTGCTGCCAGGCTGGAGTGCAGT
GCACAACTCGGCTCATGATCTCTCCGCTCCGGGTTCAAGTATTTCTCATGCTCAGCTCCTGATGATGAGT
GGATTACAGGCTCCTGCCACCGCCAGCTAATTTTGTGTTGTTTGGAGACAGACTTCGCTATTTGCT
ACCAGGCTGGAATGATTTCACTCATCTGCAACCTTCGCCACTGGGTCCAGCAATTTCTCGCTCAGCCTCC
CGAGTAGCTGAGATTTATAGGCACTACCAACACCGCCGGCTAATTTTGTGTTTGTATGAGAGACGGGTTTCA
CATGTTGGCCAGCTGGCTGCTGCAACTCTGCACTTAGGTGATCCACTCGCTTCTATCCCAAGCTGCTGGGAT
CAGGCGCTGAGCCAGCTGCGGCGGCCCACTAATTTTGTATTTTATGAGACAGGCTTTCACATGT
TGCCAGGCTGCTCTGAACTCTGACTGACTAATCGACTGCTCGCCCTCCCAAGTGTCTGGGATACAGG
TGTGAGCCACACGCGCGGTACATATTTTTTAAATGAATTTCTACTATTTATGTGATCCTTTGGAGTCAGACG

[illegible]

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FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNQSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHLRRKSP
ASGQGPNCNVKAPLGSPPSRPRRAKRFASLSRFVETLVVADDKMAAFHAGLKRILLTVMAA
AAKAFKHPISIRNPVSLVTVTRLVILGSGEEGPQVGPSSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPKDYDADRQCQLTFGPDSSRHCPQLPPPCAALWCSEHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNI PQAGGWGPGWPGWDCSRTC GGGVQFSSRDCTRPVPRNGGKY
CEGRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPFGMDWVPRYTGVA PQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSTPDVVLPGAVSLRYSGATAASETLSGHGFLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTRPPTPQDWLHRRRAITLILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGATTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTAGAAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACCTTCTTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATTCCAAAATTCGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATACAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGCTTCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCC
GCATGCTGGGGAGGGCTTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFYSGEKKKIYMEIDPVRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMPLDERGYCCICYRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAAC TGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGGCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
GCTCAGCTTCTTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCACTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
GCGCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTTGGT
GGCACCTGCTTTGCCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGGCC
CAGGGCCACCACGACCACTGCAAAACCCGCACCTGCCTACCAGCCACAGCTGCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGCTACAGGCTGAACGACTACGTG
TGAGTCCCAACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
AATGGAGGCAGGGGTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
AGCTCTCTATACCAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATATATATAT
TTATGTGGGTGATTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
TGTTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTTATGAAAAAAAAAAAAA

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FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKTRCAKGTPAKTTFAILGGTL
 FILAGLLCMVAVSWTTNDVVQNFYNPLPSGMKFEIGQALYLGFISSSLIGGTLLCLSCQ
 DEAPYRPFYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCACCACCACATGCCAAGTGGTGGCGTTCTCT
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCTCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTCTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
GGCTGGGTGGGATGGTGACAGCTGTTCCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGTG
GCATGGGTGCGTGGAGGCCCTCACATAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
CCTGGCACCAAGAAACCACTACAAGCCGTTTCTTATCATGCCCTCAGGCCACAGTGTTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAACAAAGAG
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
TGTGTAAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
AACAAAGGAGATCCCATCTAGATTCTTCTTCTGCTTTTGA CTACAGCTGGAAGTTAGAAAAGC
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCCTCAGTCTCTGTCTCTAAATATTCC
ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
ATTTTGATGATTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
TTTCCCAGCTTATCCCCAAGAAAACTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT
CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCATGATCTCGGTTTTCTTACACAT
TGATCTTAAAGTTACCAAAACCAAGTCATTTTCAGTTTGAGGCAACCAAAACCTTTCTACTG
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGCTCAGAAATTGTCCCTAGATGAATGAGAAAAATTATTTTTTTTAAAT
TTAAGTCCTAAATATAGTTAAATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
TCCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA
ACTAATTCTTTAA

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FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG
GAGTCCAGCTGGCTAAAACTCATC^{CC}AGAGGATA^{ATG}GCAACCCATGCCTTAGAAATCGCTG
GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCCTCAGTGG
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTG
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGC^{AAA}ATCTATGATTCCCTGCTGG
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGCTGATGTCCTTC
TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCCT
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
GATACTCGATACCTTCCCATCGCACACCCAAAAAAGTTATCACCCGGAAGAAGTCA^{CCG}
AGCGTCTACTCCAGAAGTCAGTATGTTAGTGTGTATGTTTTTTAACTTTTACTATTTAAAGC
CATGCAAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA
CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAA
GCTATTTACAGCAGAATGAGATATTA^{AA}CCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTTACTTCAAAATGACATTGCT
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG
TCCATTACACTGAATAAATAGA^{AA}CTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA
AGATTAAAATGAAGGCTTAAATCAGCATTGTAAGGAAATGAAATGGCTTTCATGATGCTG
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTCTCCCAGAGGCTTTTTTT
TTCTTGTGATTA^{AA}TTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCAATTCA
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
GTTTTAGGAAAGTGA^{AA}ATATTTTTGTTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
AATATAAATAAAAGAGCAGAAAAATATGCTTGGTTTTTCATTGCTTACCAAAAAAACAACA
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAA^{AA}TTG
TCATTTTTGTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTAGTTTTACTAAA
ATCTGTA^{AA}ATACTGTATTTTTCTGTTTATCCAAATTTGATGAAACTGACAATCCAATTTGA
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
TTAATAAATTTGACATTTTTTCTAATT

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FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCACTGCCCTCCTTGTGGCCCTGTTCCGGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTAACACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCTGGTGCTCACCTCTGGGA
TTGTCTTTGTCACTCAGGGGTCCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGAC**GTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTTTCTGCCTCCTGCTATTTTCTTTTGACTGAGGATATTTAAAAATTCATTT
GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCTCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCCTGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGTCCTGATAAGACG
TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCTGCCCCCCCTGCTCTACCCCCCTTACACTCACATTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

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FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPAIRSGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGTCTCTTGTGGCTCTCCCGCTGCCCTGGAACAGCCCGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCAGATGCACA
GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCTCTTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGCTCTTCTCATTTGGAGGGGGTCTGCTTTGTGGATTTTGTCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAAGCTCTCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTTGTG
GACCAATCGTGCTCCAATTTTCATATTCTAAATCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGLLCGFCCCNRRKQGYRYPVPGYRVPHTDKRRNTTMSKTSYSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

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FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATG**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTGAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGLLLLLCTVVYFCSSEEAASLSPKKVDCSIYKKYPVVAIPCFITYLPVCGSDYITYGN
ECHLCTESLKSNQVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATGG**GCTGCCTCCCCGCGCGGCTTGTGTCTTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTCAAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

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FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRRDRNGHEYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTACAGGACCCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTCACAGCAACACCGCCAG
CCCCGGACTCCCCCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCTCAATGATTACAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAGGACCCAGTTTCCCAGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCTGTGCTCCTGTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCCTGGCCGGCTTACACCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGGCCCTCC
GGACCTTGCTCCCCGCGCCGCGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCCCGCAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCGCA
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCGGGCAGAGCCG
GGCCGCCCGGGGGCCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCTCCAATCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGGTGGGAGGCTGGTGAAGGGGAGCGGGAG
GGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAA
AAAAA

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FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLGDDTQTLGSLHLPNCVLHCHVSTRVGGPPNPCCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCTTAAGAACCATCAGCCC
 TCAGTGCACCTCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCCTGGCTTTTGTG
 AAGCAGAGTTCAACATATCAAGATAAATGAAATCGGGATGGAAGCTTTGACTATGGCCTC
 TTCAGATCAACAGCCACTCTGGTGCAACGATTATAAGAGTTACTCGGAAACCTTTTGCCA
 CGTAGACTGTCAAGATCTGTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
 TTGTGTCCGGAGCAGGGGGATGAACACTGGGTAGAATGGAGGTTCACATGTTTCAGGCCGG
 CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGATGGAACAGGGTGGGGTGCACCGTGG
 AGTCATTCGAAGACTCCTGTCTCTACTCAGGATTCTTCATTCTTCTTCTCTACTGCCTCCA
 CTTTCATGTATTTTCTCCCTTCCCATTACAACATAAACTGACCAAGAGCCCCAGGAATAAA
 TGGTGTCTTGGCTCTCCTTAAGTCTCCCATCTGCACCCAGTCCCGTGTTCTCTGTAT
 TTGTAATCTGAGGACCAATAATGAAAGAAATCTTATATTATTCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGLSDWLCCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNNLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

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FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAAACTTGGGTCTCTGTGGTTTTCTGATGTGAAGTGGGAAGCAGGTCTTGCACACGC
 TGTGGCAAATGTCCAGGACCAAGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTTCTGTCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCTCTGCTGCTCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCCCTGCACACAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCACAGGATTGGGATCTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCACAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGAGGTCTCTGAAGAAGAGGAGTTGACCCCGTTTCAGCTTGGACCCAC
 GTGGCTCCAGGAGGCATCACTGCCCCGATCCCCCTCCAGAGGGCTCTGCCGAGGTGCCG
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCTCTGT
 TTTCCATGATGAGGCCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCTCTGCACACAGTGC
 CCAGGGCCTTCTCTGAAGGAGATCATCTCTGTGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGATGCTGGGGGCCACCAGGCCACCGGGGATGTGCTCGTCT
 TCATGGTGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGACGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTGCGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCGAGAGGTTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTCAAGGCCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCCCTGAGGAACAGGGTTTCGATTTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCACAGGGCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTGCGACATTCACCTGG
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCGAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAAGGGGACATCTGGGGCT
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACTCGACGACACCCAGC
 AGGAAGGAGATTCACTTTGGCAGGCCACAGCACCTGTGCTTTGCTGTCAAGCAGGAGCAGGT
 GATTCTTCAGAAGTGCACGGAGGAAGGCCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTCCACATTTCTTGGGAAATGCATGGGAAGCTGTGGTGCAAGAAAAC
 AATAAAGATTTGTACCTGCGCCGTGTGATGAAAAGCCCGCCAGCAGTGGCGATTGACCA
 GATAAATGCTGTGGATGAACGATGGAATGTCAATGTCAAGAAAGAAAAGAAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATGACTGCTGGCTGCTTA

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FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGE EYSPLEGLPFFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTFPSLDPRGLQEALSARIP LQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKR LGAIRARMLGATRATGDVLVFM DAHCECHPGWLEPLLSRIAGDRSRV VSP
VIDVIDWKT FQYYPSKDLQRGVLDWKLD FHWEP LPEHVRKALQSPISP IRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGH IYQNQDSHSPLDQEATL
RNRVRIAETWLG SFKETFYKHSPEAFSLSKAEKPCMERLQLQRRLGCRT FHWFLANVY PEL
YPSEPRPSFSGKLHNTGLGLCADCQAE GDILGCPMV LAPCSDSRQQQYLQHTSRKEIHF GSP
QHLCF AVRQEQVILQNCTEEGLAIHQH WDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

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FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAACTGGGTACACAGCTGAGGAAGACCTCAGACATGGGA
GTCCAGGATGTGGCCTGCGCTGCTGCTGCCACCTCCTTCCCTCTCTGGCCACTGCTGTTGC
TGCCCTCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACACGCCCCAGCC
CGCCCCCGTGTGCCAGGGGAGGGCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC
ACCTCCACCAAGCCGATCTCTCGGGTCCCAAGATCACGTGCGGCAAGTCTGCTTGGCACTG
CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT
ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
ATTTCTGGACTATGGTTTTGACGCCCTCATGGGCTCGCAACCCCAACCCCACTCAGACT
CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCTTGGCGGCCATT
CTGTTGGGGGGCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTACAAATTACCATCTCCAT
CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCCACCCC
TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG
CTTCTCCAGTTGAACCGGTGAGGGCAGGGGCAATGGGATGGGAGGGCAAGAGGGAAGGCAAC
TTAGCTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGTGGGAGGCAGGGCGTGGC
CTCCACAGCCCTTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTT
CTTCTCCAGCTCTCTCAGGATCTGTGCTCTATTCTCTGCTGCCATAACTCCAACCTGTCGCC
TCTTTGGTTTTTTTCTCATGCCACCTTGTCTAAGACAACCTTGCCCTTTAACTTTGATTCC
CCTCTTTGTCTTGAACCTTCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT
TCCCTTCTCTCTCAGGATTTCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGC
AAGCAGGAGGCCAAGGGGCCGCGCACAGCCCCCATCCCCTGAGGGTGGGGCAGCTGTGGGGA
GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCCGAACACTCCCCAGCC
CCACGGGCAATCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCCTCATATCTGTGACTTCG
GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGACACTCACTCCCTCACCTTAC
AGGCCATTGACACGCTCTGCACCTCTCCCGTCCATACCGCTCCGCTCAGCTGACTCT
CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCACATTCTGTGCTCAGCTCACTCAG
TGGTCAGGTTTTCTGCACACTTTACCTCTCATGTGCGTTTTCCCGGCTGATGTTGTGGTGG
TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTCCCGAGCCCTGC
GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCTTGGGGCCCTCATCGTTCATGG
TCTCGTCCCATCCACACCAATTGTTTCTCTGTCTCCCATCCTTCAAGGATGCCGGCA
TCACCGTGGGGCTCCCGCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
CTGTGTAATACTGTTTTCTGACAGATGGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA
AGGGACTCCCAATTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTGTCTGCTGCTGCTGCTG
TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCTCCTTCCCGAGCT
CCCTTTGGGCTCCCTTAACCTCACCTAGGCTGCCAGGACCCGAGTCAGCTGGTTCAAGGCC
ATCGGAGCTCTGCCCTCAAGCTACCCCTCCCTTCCCGGACTCCCTCTGTCCTGCTCCCTT
CCTCCCTCCTTCCCTTCACTCTCCTTCCCTTTGCTTCCCTGCCCTTTCCTCCCTCCTCAGGTT
CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTCCTTCCCTTCCCTTCCCTGGCTCCTAGGCT
GTGATATATATTTTTGTATTATCTCTTCTTCTTCTTGTGGTGATCATCTGAATTACTGTG
GGAATGAAGTTTCAAAATTTTCAATAAAGCCTTTGCAAGATAA

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FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 205

GTTAACCAAGCGCAGTCC'TCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGGATGG
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGGT
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGCCCCCGTGGAGAGCACCAAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
 GCGGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGCTGCTGGCGCTCGTGGTCTGCGCGCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA
 GGGGCCGCGCCCGGCCGCGCGGCGGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPDSTAQERLDQGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGC GCGGCTGAAGGTTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGCATGCGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCTCGTGGTGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGGACCTCCCCTAAGTAGCCCC
CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCAGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACAGGCCGCAT
CGACTGTGACGACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
ACTCGCAGCTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGCCCTACTGTCCCTGGGGTCCAGGCTCTCCTTGAGAGGGGGCTCCCCGCTTCCAC
CTGGCTGTCTCGGGTAGGGCGGGGCGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCTCGGCGCAGTGGAAAGTCAAGTGTCCAGGGCCTCCTGAACACATAAATAAC
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGCTCCTAGAGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCCTTTCTCCCTCAAAG
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGTTCCCATAGGGTCTGGTTCC
ACCCCATCCAGGTCTGTGGTCAAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGAGGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGTTAAGGCCGC
CTGAGCTCGGACTCAGGGGGAGGGGGTTAAAGGAGAGAGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGACAGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTAC
CTCTGCAACCACACCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCTGCACACCCTTCGGACATCCAGGC
ACGAGGGTGTCTGTGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGTGTGCTGC
CTCAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCTGGGCAGGTCCGACAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTCTC

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FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDL P

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGAAGCTGCCCCGTCCAGGTTCATGTTCTCTTATTCTT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACCCATCTGCCTCTTTCGCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCTCTCTCTGTATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAAACTTTTGTGATGGATTCTTAAGTGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGAACTTCTCTCTTGGAACACTACATATGGCC
 AAGTATCTACTTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGACGTGCACACACGACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCCTGTCTTAAATCTCGTTTCTC
 TTCTTCCTTCTTTTAAATTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTTATAAGCACATGTCCTGCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTTAGCATCTCCAACCTCCC
 TATGTAAATCAACAACCTGCATAATAAATAAAGGCAATCATGTTATA

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FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTQVPAAMEFIAATEVAVIG
FFQDLEIPAVFPLHSMVQKFPVGSFGISTDSEVLTHYNITGNTICLFRQLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQKGILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGGCGGGCGGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGGCGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCTGTAGAAAAAGAGAATTGGCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTTGTACCAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAGAAGAATACCTAGAACATATC
CTCAGACAAGAAACAAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTAGAAAACATTCCCTTACCACATCATTTAGAAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCCTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
AAATGTGTCATATCAATTTCTGGATTCAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACCTTCACTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
GAGAACTTTTGTACGTGGAGAGTAAAAAGTATCGGTTTTTA

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FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop .

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGGCCCCGGCGCAGTCCCCCGGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGATC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACC GTTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAGAAGAGAAAGCTTATAAGCCTTGAAGATGA
 TGAAGAAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTAAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTTGTATTCA
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAGGTGAAGGAAGTAAACA
 TGTTTATAAAGTAAAAAA

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FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQEQSLAPWSPQTPAPPSCRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEKEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGCGCAGCCAGCGCTGGGGCAACCCGGGTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGTCTCCCTGG
 TGGAGTCGCACCTGTTCGACCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTGCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAAGGCCAAGAACCCCGAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGTCACTTGATACGTTATTTCAGAAACCCAAG
 GAATGGCTGTCCCATCTCATGTGGCTGTGTGGAGCTCAGCTGTGTGTGTGGCAGTTTAT
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

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FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
 DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRI PRRPGALDGLEA
 GGYVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
 LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
 GGGGGGGGGGSGLCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGCAGCAGGTCTGTCGGGGGCCACAC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
GTCAAGATCGCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
AACTGGACTTCTATCAGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
CTCTATAAACTCTACCAGCATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
GCAAGAATTCTTTGTGCTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCAGTGGAACGGCATGACTTCCCTGCTGAGT
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCTGTAGCGCCCTTGTGGCTGC
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCCTGCTCCTGTGCGACCGCCGC
GTGCTGCTGCTGGGCACCATACAAGCTCTATTGAGAGTGTATCTTCATCTTTGTCTTCCT
CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
CCCATGCACCTGCTGTCCCTTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT
CTCTACCAGCCCAGGCCAGGAGTCCGGTGGAGTCCCTTCATAGCCTTTCTACTTATTGAGT
TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA
GAGCAGGCTGGTGACTCACTGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACCTCGGAATATGTTACGACTTGTCTG
CTGTCTGCTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTGT
GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCATTAGAAA
ATAAACACTTTTAAATGATCAAAAAAAAAA

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FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
 VLLGLTIQALFESVIFIVFLWTFVLDPHGAPLGII FSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSFLMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
 EQAGVLNWFVRVPLHSLACLGLLVLHSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
 ELRVSPSTEOPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGCGGCGAGAGGAAACGCGGCGCGGGCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGCGGGCTGGTGTCTCGTGCTCTGGTCCCCGCGTGCGTCGCGGCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCTCCGCTGAACCTCCAGAGGCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCAACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGT**TAGA**AAGAGTTTGTCCACATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGA
AAAGGTTTGGCGTTGTCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
GCTTCTCATCAGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

[illegible]

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FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop .
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPHYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNnkSSIHCMDLSQRYCLMAVFNVIIYLENEDSE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCAACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTACGACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTGCG**CTAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACAGTGCAGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

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FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSEQEGQVLVGIYGQYQLLGIIKSIGFEWNYPLEEPTTEPPVNLTYANSVPGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAAC TGGGTGCTCATCAGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTAAACCGCCCCCTCCCCACCCCCCAAAAAAAGCTGTAAGAGATGCAAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCAAGGGGTCCAATTTTTCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTGATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTCGGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTACCGAGGAATGTCTTTGCTGGC
 ATGACTCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAAGCCTTCAGAACCTTTACTTGCACTGGAATAAAATCAGTGTATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCCTCAACCTGGA
 TTCCAACAAGCTCAATTTATTGGTCAAGAGATTTTGGATTCTTGGAATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTGTAACTGGCTG
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATATATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAGCCGACGTTTAAAGCCCAAGCTCCCAGGGCCGAAGCAT
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCCATAAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCCAGCGAGA
 TGCTGCTGAATGGGACGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTTGTATAAAAAGAGCTCTTAAAGCTGGGAATAAGTGGTGCTTTATTGAATC
 TGGTGACTATCAAGGGAACCGGATGCCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTTGTCCGTTTTAGTGCATTATAATACCTGGTCATTTTCCCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCGGTTTAATATAA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAAATGTGCACTTTGTTTTAAGATAAAAT
 TCTTTCATAGGTAAAAA

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FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCGKMGVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLKLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKLHLEHNQFSKLNLAFLPRLVSLQNLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPLPPTVGATEPGPETDADAEHISFHKKIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAATATGTC AAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGCACCATTGGCAGTTTTTGTGTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATGTGA
 AAAACAACCTGA TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGAGGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTTTGGCAGTGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

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FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRPRIDSHRRTMVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGCGCTCAGAAGCTCCGTGGCGGCGCGACCGTGACGAGAAGCCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAGTCAGATGCCCTTTTAAACT
 CCCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGCTCTTGATTGTGGC
 TTACCTCAAGTTACCATTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGCTTTTTTA
 CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGTTATTTGGACTCATT
 TGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAATTAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT
 TGTGTGTAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTATGGAAC
 TCTAATTCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTTTCAGGCAAGCTGTTCAATG
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCT
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAAATGTTTAA
 CTATTCTGTCATTTGTTCTAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTGTTATTTCCAAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAAATGTATTGTTGCACTATCCTTCAGAATAACTGA
 AGGTAAATTATTGTATATTTTTTAAATTTACACTATAAGAGTATAATCTTGAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAATAAGTT
 GTAAACTCTAATCTTACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTACATACATGAATGTTTCATTTAAAAGTTTAACTCTTGAGTGCT
 ATGCTATCAGGAAAGCACATATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTACATTATATTATATAAGAGTATC
 CTTTATGAAATTTGAAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCAGAGGGAACCCATCTTGGGTAATTCCTAGTATAAAAACAAATTACTTTTAT
 TTAATTTCCCTTGTAAGCAAACTAATTGCCACATGGTGCCCTATATTCATAGTATTTATT
 CTCATAGTAAGTCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
 TGTATTGTTCTGCTATTATAATAGTACCACATGTAGCAATAATTAACAATTTTTATTAATAA
 TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAATCTCTCTTCTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

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FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop .
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTINKRTINVSGSIR
```

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGCGCGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCCAGACAACCCGGCCATGCT
 TCCCGGGTGCCAAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCTGGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGCTCCTCAACCCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCGGGCT
 ACACGACGTTGGCTGGCTGGATCTCAGCACAACCTGTCTCACCAGCATCTCACCACCTGCC
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTACCAGCTCACCCTTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCATACAGCTGGACCTCTCC
 CACAACCTCATTACCAGCCTCGTGCCCCACCCACGAGGGGCGGGCTGCTGCGGCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCTC
 TGGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATTGGTCCGGGTGCCTTCGCGGGG
 CTGGGAGGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCGTGAGCTACCGGCCCTGCAGGTCTTGACCTCTCGGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGTGTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGACCTTTCGGGCAAC
 AACCTGGTGCCCTGCCTTGAGCGCTGTCTCCTCCACTCCCGGCACTGCAGAGCGTCAGCT
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGGGGAGGGCACCTACCCCGGAGCCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
 ATCT**TGTA**CAAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCTCAG
 GTCCCGAGTAACTTATGTTCAATGTGCCAACACCACTGAGGGAGCCCGCAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTACCCCCTTGTCTACGTGTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCAAGTGCTTCCCTCAT
 GCCTGGGCGGCCCTGACCCGCAATGGGCAGAGGTGGGTGGGACCCCTGTGCGAGGGCAGA
 GTTCAGGTCACCTGGGCTGAGTGTCCTTGGGCCCATGGCCAGTCACCTCAGGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTTCATGTGAC
 AGATGGGGAACCTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCTCCTGCCTCCAGCCCGGACCCCAATGCACCTTTCTTGTCTCCTCTA
 ATAAGCCCCACCTTCCCGCCTGGGCTCCCTTGTGCTGCTTGTCTTCCCATAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGACCTCACAAAGTGGGACTCTGGGCCTCTGACCAGCT
 GTGCGGCATGGGCTAAGTCACTCTGCCCTCGGAGCCTTAGGGCACTTAGGCTTATGGTT
 CCAGCCTAGCCAGTTTCTCACCTCGGGTTGGGGTCCCCAGCATCCAGACTGGAAACCTACC
 CATTITCCCTTGACATCTCTAGATGCTGCCCGCAAGGAGTTGCTGAGTTCTGAGGCTCA
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTCACTCCCACTGGCCCTGAGCACGACAGC
 CCTTCTTACCTTCCCAGGAATGCCGTGAAAGGAGACAAGGCTCTGCCCGACCATGTCTATGC
 TACCCCCCAGGACGACATCTCAGCTTCCGAACCTGGGCTGTTTCTTCTAGTCTCATTTTA
 TAAAGTTGTGCTTTTTTAACGGAGTGCTCACTTTCAACCGGCCTCCCTACCCCTCTGCG
 CGGGATGGAGACATGTCACTTTGTAAAGCAGAAAAAGGTGTGCTTCACTTTGTGTAAT
 ATTGTCTTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC
 CCATCATCTATCTAACCAGGTCTTGTATTTAATAAACACTATAAAAGGTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop .
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSATTHSQGRALHVDLSHNLIHRLVPHPTAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCTGTGGGTCTGAGG
GGACCAGAAGGGTGAAGTACGTTGGCTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCAGTGCAAGTGCCTGCT
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTTTCAC
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTAGGCTTAAGATGAAAGCC
TCTAGTCTTGCCTTCAAGCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
GCTAAGACTCTATCTGGACAGGCTATTTAAAACTACCAGACCCCTGACCATTATCTCTCC
GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGTGCTGCTGCTAAGAATATTCGAGGT
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCTTGCATGAT
TGTCCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTT
TCTGCTATTTGGATATATTTATAGTTAATATATTTATTTATTTTTTGTATTTAATGTATTT
ATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTATAAACCCTGACTAG
AGCAGGTGATGTATTTTTATACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
AGGGGGTTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
CCAAAAAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPVAVPGLTCWALTAEPGWGQNGKATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSEFLTICKDLRLSHAHMTCHCGEAMKKYSQILSHFEKLEPQAADVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCC
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACGACCTAGTGAAGGTTGAGATGCAAAAT
GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTTCGTGGTGATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCAGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTATCAAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTTAA

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FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLNTPLEDNIMTHGLSSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT
TGAGTTTGAATAGTTTTATGAAATTTCTTTATTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCCTCTAGCCTGGGGGAGAAAGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAGA
AAAAATATTGTTCTTATGTATTGAAGAAGGTACTTTTATATAATGATTTTTTAAATGCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

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FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVGILFFTGWWMIDAADVYPKPEQLNHAFTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGGCCAGGGTGGT
 GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATCCGGGGGGTGCACTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACCAAATGAACGATGAAAGCAGGAAATCTTCTCTGACTTG
 GGGAGTTCCTACGAAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAGAACAGCCAGACACAAACAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTGCGCCCTCTCCTCCTCGAAACAGAACCCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGTTTGTGAAAAA

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FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
 ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
 DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRLFSDLGSSYAKQLGFRDSWVFIGAKD
 LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTGCGGGAT
CCAGAAAACCATGATACCTTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACA
GCAAGAGAAGCAGAGATAAATACACTCAGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATCCCAGTCCC
CTGCACCCCTTCTCTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCC
TGGCTGCAGATGGGGGTCAACTGAGCTATGAGGGCCACATGGTCAGGACCATTGGCCA
GCCTCTTACCCTGAGTGTGAAAACAATGCCAGTCGCCATCGATATTACAGACAGACAGTGT
GACATTTGACCCTGATTTGCTGCTCTGCAGCCCCACGGATATGACAGCCTGGCACCAGAGC
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTGTCAGAGCTCCACATTGTAC
ATTATGACTCTGATTCCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
TCACTTGACATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCAGATTTCAATGGAACAGCT
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
ACTACCAGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTCTTTTCATCCAAGCAGGA
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
CCTTCTCTGGCTGTTTATTTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA
AGAGTGTGGTCTTCACTCAGCACAAAGCCACGACTGAGGCAATAATTCCTTCTCAGATACCA
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGGTAGGATCTG
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCTGGACATCTCTTAGAGAG
GAATGGACCCAGGCTGTCACTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTGTGTGAGGG
GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTCCCTAGATA
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGATCAATA
TATTTGGAATTAAGTTTCTGACTTT

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FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLL
FSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSUVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible]

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FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGGCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCCTCCAGCTCCGCGCTGCCCG
GCAGCGGGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGGCTCC
TGCTGCTCTGTGCTGCAGCTGCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCCTTGGAG
GAGTCTTGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGTCTAAGAGTTTTGT
TCAGTGGCTCAC TTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTC
AATGGAGCTGAATGTTTCAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
CCCTGAAATGAATTCACAATTAATATTCATCGCACTTCTCTGTGGAAGGACTTTGTGAAG
GAATTGGTGTGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACACCAAAAAT
AATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACCTAAAT
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTTCATTTTGCTTCAATCAAAGT
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
TAATTTGGAATATTTGTTGGTCTTTTGTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA
TAAAGCTACCAATCTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT
AAAAATTATTTCCAACA

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FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVPIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYILDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217